

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2001, 23:31:06 ; Search time 2385.2 Seconds
(Without alignments)
8715.686 Million cell updates/sec

Title: US-09-670-568B-2_COPY_145_1488
Sequence: 1 atgtccacagacacacagac.....caacacgtcagtaccaca 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_ba3: *
4: gb_in1: *
5: gb_in2: *
6: gb_in3: *
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12: gb_pl1: *
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14: gb_pl3: *
15: gb_pl4: *
16: em_ba1: *
17: em_ba2: *
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21: em_higo_rod: *
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23: em_hig_hum2: *
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92: gb_pr8: *
93: gb_pr9: *
94: gb_rod1: *
95: gb_rod2: *
96: gb_in4: *
97: gb_pr10: *
98: em_ba3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1344 | 100.0 | 1347 | 88 AF075428 | AF075428 Homo sapi |
| 2 | 1344 | 100.0 | 2816 | 85 AB016072 | AB016072 Homo sapi |
| 3 | 1232 | 91.7 | 1351 | 88 AF075432 | AF075432 Homo sapi |
| 4 | 1232 | 91.7 | 1926 | 88 AF075430 | AF075430 Homo sapi |
| 5 | 1232 | 91.7 | 2031 | 89 AF116771 | AF116771 Homo sapi |
| 6 | 1232 | 91.7 | 2270 | 85 AB016073 | AB016073 Homo sapi |
| 7 | 1232 | 91.7 | 4846 | 9 AX009538 | AX009538 Sequence |
| 8 | 1232 | 91.7 | 4849 | 92 HSA16961 | Y16961 Homo sapien |

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QY 901 ttggaagccggatctgtctgtcccaagaagaagaagcggatgaagaatcagtc 960
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DB 1321 CCCCCAACCGATCTAGTGTACCCA 1344

RESULT 2
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DEFINITION Homo sapiens mRNA for p51A, complete cds.
ACCESSION AB016072
VERSION AB016072.1 GI:3510327
KEYWORDS p51A.
SOURCE Homo sapiens skeletal muscle cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2816)
AUTHORS Ikawa,S. and Osada,M.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-1998) to the DDBJ/EMBL/Genbank databases.
Shuntaro Ikawa, Institute of Development, Aging and Cancer,
Department of Cell Biology; 4-1 Seiry-machi, Sendai, Miyagi
980-8575, Japan (E-mail:sikawa@idac.tohoku.ac.jp,
Tel:81-22-717-8484, Fax:81-22-717-8488)
2 (sites)
REFERENCE Osada,M., Ohba,M., Kawahara,C., Ishioke,C., Kanamaru,R., Katoh,I.,
AUTHORS Ikawa,S., Nimura,Y., Nakagawara,A., Obinata,M. and Ikawa,S.
TITLE Cloning and functional analysis of human p51, which structurally
and functionally resembles p53
JOURNAL Nat. Med. 4 (7), 839-843 (1998)
MEDLINE 98324755
FEATURES
source Location/Qualifiers
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Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 205 GATTTTGTGAAACGCTTATGTTCAGTTTCAGCCATTGCACTTGTGTGATGAA 264
QY 121 ccatcagaagaatgttgagacaagaatgagaattgacatgagactgtatccgcatgag 180
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DB 565 TCCYTCACGACGAGTGCACACCGCCAGCGCCACCTGAGAGTTCACAGAACTGAG 624
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RESULT 4
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 LOCUS AF075430 Homo sapiens TA p63 alpha mRNA, complete cds.
 DEFINITION AF075430
 VERSION AF075430.1 GI:3695081
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
 AUTHORS Yang, A., Kaghad, M., Wang, Y., Gilliet, E., Fleming, M. D., Dotsch, V.,
 Andrews, N. C., Caput, D. and McKeon, F.
 p63, a p53 homolog at 3q27-29, encodes multiple products with
 transactivating, death-inducing, and dominant-negative activities
 Mol. Cell 2 (3), 305-316 (1998)

TITLE
 JOURNAL
 MEDLINE
 REFERENCE
 AUTHORS Yang, A., Kaghad, M., Caput, D. and McKeon, F.
 TITLE Direct Submission
 JOURNAL Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240
 Longwood Ave, Boston, MA 02115, USA

FEATURES
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DEFINITION Homo sapiens p51 delta mRNA, complete cds.
ACCESSION AF116771
VERSION AF116771.1 GI:7384975
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 2031)
Tani, M., Shimizu, K., Kohno, T., Ikawa, S. and Yokota, J.
Mutations and expression of the p51 gene in human lung cancer
unpublished
2 (bases 1 to 2031)
Tani, M., Shimizu, K., Kohno, T., Ikawa, S. and Yokota, J.
Direct Submission
Submitted (28-DEC-1998) Biology Division, National Cancer Center
Research Institute, 1-1, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045,
Japan

FEATURES
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CDS

BASE COUNT 543 a 591 c 454 g 443 t

ORIGIN

Query Match 91.7%; Score 1232; DB 89; Length 2031;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 205 GATTTTCTGGAACAGCTTATGTTGATTCAGTTCAGCCCATGACTTGAACCTTGTGATGAA 264
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| LOCUS | AB016073 | 2270 bp | mRNA |
| DEFINITION | AB016073 | Homo sapiens mRNA for p51b, complete cds. | PRI |
| ACCESSION | AB016073.1 | GI:3510329 | 06-FEB-1999 |
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| KEYWORDS | | p51b. | |
| SOURCE | | Homo sapiens skeletal muscle cDNA to mRNA. | |
| ORGANISM | | Homo sapiens | |
| REFERENCE | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | |
| AUTHORS | | 1 (bases 1 to 2270). Ikawa,S. and Osada,M. | |
| TITLE | | Direct Submission | |
| JOURNAL | | Submitted (10-JUL-1998) to the DDBJ/EMBL/GenBank databases. Shuntaro Ikawa, Institute of Development, Aging and Cancer, Department of Cell Biology; 4-1 Setryo-machi, Sendai, Miyagi 980-8575, Japan (E-mail:sikawa@idac.tohoku.ac.jp, Tel:81-22-717-8484, Fax:81-22-717-8488) 2 (sites) | |
| REFERENCE | | Ikawa,M., Ohba,M., Kawahara,C., Ishioka,C., Kanamaru,R., Katoh,I., Osada,Y., Minura,Y., Nakagawara,A., Obinata,M. and Ikawa,S. Cloning and functional analysis of human p51, which structurally and functionally resembles p53 Nat. Med. 4 (7), 839-843 (1998) 98324755 | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| MEDLINE | | | |
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| SOURCE | | location/qualifiers 1..2270 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="3" /map="3q28" /tissue-type="skeletal muscle" 145..2070 /codon_start=1 /product="p51b" /protein_id="BAA32593.1" /db_xref="GI:3510330" /translation="MSOSTQNEFLSPPEVHOIHDFLEQPCISQVPIIDANVEDPSED GATNKEISMCIKRMQSDSDPMPWPQITNLGLNSMDQIQNGSSSTSPNTDHAON SVASPSYAPQPSSTFDALSPSPALVISMVDYPGPSFVSEFOQSTASATWTYSTELK KLYQIAKTCPTQIKVMTPEPGAVIPMAMPEYKKAHEVTEVRCSPNHELISREFNEGQ IAPSHLIRVGNHQAQVEDPITGRQSVLVPYPPQVGFETVLVLFMKNSSCVGSG MNRPSLIITVLETRDGOVLGRRCFEARICACPGDRKADDSIRKQOVSDSTKNGG TKREPRONTGICQMTSIRKPSPPDELLIYPRRERYEMLIKIKESLELMQYIPQIT IETRYQQQOQHHLAKQTSIOSPSYSGNSPPLANKMSNKLPVSVOLINPOQRNNA LTPTTIDGMGANTIPMGTHMPMAGMDNGSLSPALVISMPTSTCTEPPYPTQCS SYVEFLIARGSSCLDITFTQGLTITVQIEHYSMDLIALCIPEQFHAIKWGILDRH QLHFFSSPSHLRTPPSASVSVSSSETRGERVIDAVFTLRQITISPPREDMDNFNNE DMDARKKQOKIKKEGE" | |
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| QY 361 tctccatacccccgcataccccctccaaacacggactaccacggcccgacagagtttgacg 420 | | | | | |
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| QY 541 cctcagggagcgtgtatccgggcacatgctgtctaaaaaaagcttgagacgttcaaggg 600 | | | | | |
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| Db | | |
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| RESULT | 7 | | | | | |
| AX009538 | | | | | | |
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| SOURCE | | | | | | |
| ORGANISM | | | | | | |
| | synthetic construct. | | | | | |
| | synthetic construct | | | | | |

| | |
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| AUTHORS | Bamberger, C., Paul, D., Augustin, M. and Schmale, H. |
| TITLE | Tumour suppressor genes of the p53 family |
| JOURNAL | Patent: WO 9961610-A 2 02-DEC-1999. |

FEATURES
 BRAUBENGER CASIMIR (DE); PAUL DIETER (DE); AUGUSTIN MARTIN (DE);
 SCHMALE HARTWIG (DE); FRAUNHOFER GES FORSCHUNG (DE)
 Location/Qualifiers

| BASE COUNT | ORIGIN | |
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| 1372 | a | 1077 c 990 g 1406 t 1 others |

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| Query Match | 91.7% | Score 1232 | DB 9 | Length 4846 |
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| RESULT | 8 | | |
| LOCUS | HSAL19661 | 4849 bp | 03-DEC-1998 |
| DEFINITION | Homo sapiens mRNA for KET protein. | | |
| ACCESSION | Y16961.1 | | |
| VERSION | GI:3970716 | | |
| KEYWORDS | KET gene; KET protein. | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | |
| REFERENCE | 1 (bases 1 to 4849) | | |
| AUTHORS | Schmale,H. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (24-MAR-1998) H. Schmale, Institut f. Zellbiochemie und Klinische Neurobiologie, Universitaetskrankenhaus Eppendorf, | | |

REFERENCE 2 (bases 1 to 4849)
 AUTHORS Augustin, M., Bamberg, C., Paul, D. and Schmale, H.
 TITLE Cloning and chromosomal mapping of the human p53-related KET gene to chromosome 3q27 and its murine homolog Ket to mouse chromosome 16
 JOURNAL Mamm. Genome 9 (11), 899-902 (1998)
 MEDLINE 99018225
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 LOCUS AF075429
 DEFINITION Homo sapiens DN p53 gamma mRNA, complete cds.
 ACCESSION AF075429
 VERSION AF075429.1 GI:3695079
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1182)
 AUTHORS Yang, A., Kagnad, M., Wang, Y., Gillett, E., Fleming, M.D., Dotsch, V.,
 Andrews, N.C., Caput, D. and McKeon, F.
 TITLE p53, a p53 homolog at 3q27-29, encodes multiple products with
 transactivating, death-inducing, and dominant-negative activities
 JOURNAL Mol. Cell 2 (3), 305-316 (1998)


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RESULT 12
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LOCUS AF075436
DEFINITION Mus musculus TAP63 alpha mRNA, complete cds.
ACCESSION AF075436
VERSION AF075436.1 GI:3695093
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 2043)
Yang, A., Kagnad, M., Wang, Y., Gallet, E., Fleming, M.D., Dotsch, V.,
Andrews, N.C., Caput, D. and McKeon, F.
p53, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities
Mol. Cell 2 (3), 305-316 (1998)
JOURNAL
MEDLINE
REFERENCE
2 (bases 1 to 2043)
9848095
Yang, A., Kagnad, M., Caput, D. and McKeon, F.
Direct Submission
Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240
Longwood Ave, Boston, MA 02115, USA
JOURNAL
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RESULT 14

LOCUS AF061512

DEFINITION Homo sapiens p53 homolog (p40) mRNA, complete cds.

ACCESSION AF061512

VERSION AF061512.1 GI:3273744

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE Trink, B., Wu, L., Okami, K., Siurupong, V., Jen, J. and Sidransky, D. Direct Submission Submitted (24-Apr-1998) Otolaryngology-Head & Neck Surgery, The Johns Hopkins School of Medicine, 720 Rutland Ave., Baltimore, MD 21205-2196, USA

FEATURES

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Job time: 3905 sec

PI Wang T, Fan L:
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DR P-PSDB; AAB11359.
XX
PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -
XX
PS Claim 25a; Page 238-239; 261pp; English.
XX
CC This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
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Best Local Similarity 100.0%; Pred. No. 0;
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QY 781 acgacagctctgtacaatttcattglttaacagcagttgtgttgagggatgaaacgcgcgt 840
DB 925 acgacagctctgtacaatttcattglttaacagcagttgtgttgagggatgaaacgcgcgt 984
QY 841 ccaatttatacttctgttactctcggaaacagagatgggcaaatctctggccagctgc 900
DB 985 ccaatttatacttctgttactctcggaaacagagatgggcaaatctctggccagctgc 1044
QY 901 ttgagggccggatctgtgtgttgcggagagagacagagcgagatgagatgacatc 960
DB 1045 ttgagggccggatctgtgtgttgcggagagagacagagcgagatgagatgacatc 1104
QY 961 agaaagcagcaagtttcgcgacagtaacaagaacggtgatacgagcgccggttcgt 1020
DB 1105 agaaagcagcaagtttcgcgacagtaacaagaacggtgatacgagcgccggttcgt 1164
QY 1021 caagaacacatgtgtatccagatgacatccataagaagaagatccccaatgtatgaa 1080
DB 1165 caagaacacatgtgtatccagatgacatccataagaagaagatccccaatgtatgaa 1224
QY 1081 ctgttatacttaccagtgagggccgtgagacttatgaaatgctgtgaaatcaagaag 1140
DB 1225 ctgttatacttaccagtgagggccgtgagacttatgaaatgctgtgaaatcaagaag 1284
QY 1141 tccctggaactcatgacgtacccctcctcagcacacaattgaaacgtacagcaagcaa 1200
DB 1285 tccctggaactcatgacgtacccctcctcagcacacaattgaaacgtacagcaagcaa 1344
QY 1201 cagcagcagcagcagcagcacttactcagaacacatcctcttcagccctgattcaagatgag 1260
DB 1345 cagcagcagcagcagcagcacttactcagaacacatcctcttcagccctgattcaagatgag 1404
QY 1261 ctgttgagagcccggaagagaactccaaacaaatctgacgtctctctttagacattccaa 1320
DB 1405 ctgttgagagcccggaagagaactccaaacaaatctgacgtctctctttagacattccaa 1464
QY 1321 cccccaaccgcatcagtgatccca 1344
DB 1465 cccccaaccgcatcagtgatccca 1488

RESULT 3
AA58574
ID AA58574 standard; cDNA; 1347 BP.
XX
XX AA58574;
AC
AC 16-AUG-1999 (first entry)
DT
DT
DE Human cell regulatory protein p63, isoform huTap63 gamma, cDNA.
XX
XX Cell regulatory protein; p63; huTap63 gamma; Tap63 gamma; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy; ss.
XX
XX Homo sapiens.
FH Key Location/Qualifiers
FH msc-difference 1254
FT
FT /*tag= a
FT /note= "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to maintain
FT the nucleotide numbering given in the

Specification for this sequence"

FT XX XX M0991357-A2.
 XX XX 22-APR-1999.
 XX XX 02-OCT-1998; 98MO-US21992.
 XX XX 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 XX XX (HARD) HARVARD COLLEGE.
 PI McKeon F., Yang A.
 XX XX WPI: 1999-277595/23.
 DR P-SDB: AAY05955.
 XX XX
 PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 XX XX
 PS Claim 1: Fig 11; 161pp; English.

The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the known exon organisation is conserved between p73 and p53, and from CC identity new members of this gene family using a PCR-based strategy CC of amplifying 2 exons in a conserved domain and their intervening CC intron. The human p53 gene was localised to chromosomal position CC 3q27-29. At least 6 different isoforms exist. Splice variants CC differing at the C-terminus have been designated as alpha, beta and CC gamma forms, while p63 members differing in the N-terminus are CC designated as delta and TA forms, where the delta form lacks the CC transactivation domain. The present sequence represents a cDNA CC clone encoding human TA-p63 gamma. p63 was detected in a variety of CC human and mouse tissue. It demonstrates remarkably divergent CC activities, such as the ability to transactivate p53 reporter genes CC and induce apoptosis. Cessation or down-regulation of p63 expression CC may play a critical role in the process of cervical squamous CC differentiation, both benign and neoplastic. Delta isoforms of p63 CC act as dominant negatives towards transactivation by p53 and p63. CC p63 may also be implicated in hematopoiesis, muscle wasting (e.g. CC cachexia) and neuronal differentiation and related degenerative CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see CC AAY58572-83) and anti-p63 antibodies of the invention can be used to CC identify compounds useful for treating disorders involving such CC processes, in detection and diagnosis, and in the production of CC transgenic animals.

Sequence 1347 BP; 374 A; 381 C; 316 G; 275 T; 1 other;

Query Match 99.9% Score 1343; DB 20; Length 1347;
 Best Local Similarity 99.9%; Pred. NO. 0;
 Matches 1343; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atgtcccaagacacacagaacaaatgaattcctcagtcacagaggtttccacatactg 60
 Db 1 atgtcccaagacacacagaacaaatgaattcctcagtcacagaggtttccacatactg 60
 QY 61 gatttctggaacagcctatagtgtcagttcagccatgactgaaactgttgatgaa 120
 Db 61 gatttctggaacagcctatagtgtcagttcagccatgactgaaactgttgatgaa 120
 QY 121 ccatcagaagatgtgtgcacaacaagattgagattgagtgagctgtatccgcatgag 180
 Db 121 ccatcagaagatgtgtgcacaacaagattgagattgagtgagctgtatccgcatgag 180
 QY 181 gactggacctgagtgcccatgtgcccacagatacagaacctggggctcccgaaacg 240
 Db 181 gactggacctgagtgcccatgtgcccacagatacagaacctggggctcccgaaacg 240

Db 181 gactggacctgagtgcccatgtgcccacagatacagaacctggggctcccgaaacg 240
 QY 241 atggacagcagatcttcaagaagcgtcctgttccacagatccctatacaacagacagcg 300
 Db 241 atggacagcagatcttcaagaagcgtcctgttccacagatccctatacaacagacagcg 300
 QY 301 cagaaagcgttcaagcgcgccttcgacctacgacagacccagctccacttgatcttc 360
 Db 301 cagaaagcgttcaagcgcgccttcgacctacgacagacccagctccacttgatcttc 360
 QY 361 tctccatcacccgccttccctcccaacacagcctacccagcgcgcagagtttcgagtg 420
 Db 361 tctccatcacccgccttccctcccaacacagcctacccagcgcgcagagtttcgagtg 420
 QY 421 tcttccagcagtcgacacgcgcgcacagtcgcacactggaagtcattccatgaaactgag 480
 Db 421 tcttccagcagtcgacacgcgcgcacagtcgcacactggaagtcattccatgaaactgag 480
 QY 481 aaactctactgccaatctgcaagaacatgcccacatccagatcaagtgatgaaccacact 540
 Db 481 aaactctactgccaatctgcaagaacatgcccacatccagatcaagtgatgaaccacact 540
 QY 541 ccttcagagagcgtgtatccgcgcacatgcttcttcaaaaaagctgacgcgcagcagag 600
 Db 541 ccttcagagagcgtgtatccgcgcacatgcttcttcaaaaaagctgacgcgcagcagag 600
 QY 601 gtgtggaagcgtgtgcccacacatgagtgagcgcgtgtaattcaagagagacagatggcc 660
 Db 601 gtgtggaagcgtgtgcccacacatgagtgagcgcgtgtaattcaagagagacagatggcc 660
 QY 661 cctcttaacttgaattgagtagagagagacagcagatccagatgtagaagatccc 720
 Db 661 cctcttaacttgaattgagtagagagagacagcagatccagatgtagaagatccc 720
 QY 721 atcacaagaacacagagtggtgtgtacattatgagcaccacaggttggacatgattc 780
 Db 721 atcacaagaacacagagtggtgtgtacattatgagcaccacaggttggacatgattc 780
 QY 781 agcagagcttctgtaacatttcaatgtgttaacagcagtggtgtgagagtgagacgcgct 840
 Db 781 agcagagcttctgtaacatttcaatgtgttaacagcagtggtgtgagagtgagacgcgct 840
 QY 841 ccaatttaactatgttactctggaacacagagatggcagatccctggccgacgtgc 900
 Db 841 ccaatttaactatgttactctggaacacagagatggcagatccctggccgacgtgc 900
 QY 901 ttgagagcccgagatcgtgtgttgcacagaaagacagaaagcgagatagatc 960
 Db 901 ttgagagcccgagatcgtgtgttgcacagaaagacagaaagcgagatagatc 960
 QY 961 agaaagcagcaagttctcgacagatcaaaagacggtgtatgttaagaaagcgcgcttc 1020
 Db 961 agaaagcagcaagttctcgacagatcaaaagacggtgtatgttaagaaagcgcgcttc 1020
 QY 1021 cagaaacacatggtatccagatgacatccatcaagaagaacagaaagatcccatgatatgaa 1080
 Db 1021 cagaaacacatggtatccagatgacatccatcaagaagaacagaaagatcccatgatatgaa 1080
 QY 1081 ctgttaacttccagtgtaggggcgttgaagactatgaatgctgttgaagatcaagag 1140
 Db 1081 ctgttaacttccagtgtaggggcgttgaagactatgaatgctgttgaagatcaagag 1140
 QY 1141 tccctggaactatgtagtaccttccctcaagacaacatgaaacgtgacagcaagcaaa 1200
 Db 1141 tccctggaactatgtagtaccttccctcaagacaacatgaaacgtgacagcaagcaaa 1200
 QY 1201 cag 1260
 Db 1201 cag 1260
 QY 1261 ctgttgagcccgagagagaacatcccaaaacatctgagcttcttcttgaattccaaag 1320
 Db 1261 ctgttgagcccgagagagaacatcccaaaacatctgagcttcttcttgaattccaaag 1320

QY 1321 ccccaaacgcatggtaccca 1344
 Db 1321 ccccaaacgcatggtaccca 1344

RESULT 4
 AAX58573
 ID AAX58573 standard; cDNA; 1551 BP.
 XX
 AC AAX58573;
 XX
 DT 16-AUG-1999 (first entry)
 XX
 DE Human cell regulatory protein p63, isoform hUTAP63 beta, cDNA.
 XX
 KW Cell regulatory protein; p63; hUTAP63 beta; TAP63 beta; human;
 KM cancer; tumour suppressor; cell cycle control; apoptosis;
 KM cell proliferation; cell differentiation; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09919357-A2.
 XX
 PD 22-APR-1999.
 XX
 PF 02-OCT-1998; 98MO-US21992.
 XX
 PR 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 XX
 PA (HARD) HARVARD COLLEGE.
 PI McKeon F, Yang A;
 DR MPI; 1999-277595/23.
 DR P-PSDB; AAY05954.
 XX
 PT New isolated p63 cell regulatory protein for, e.g. treatment of
 tumors
 PS Claim 1; Fig 10; 161pp; English.
 XX

The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isootypes exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as delta and TA forms, where the delta form lacks the transactivation domain. The present sequence represents a cDNA clone encoding human TAP63 beta. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. Delta isoforms of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see AAX58572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.

Sequence 1551 BP; 425 A; 466 C; 350 G; 310 T; 0 other;

Query Match 91.7%; Score 1232; DB 20; Length 1551;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtccagagcagacagacaaatgaatttcctcagtcacagagtttccagcatatcg 60
 Db 1 atgtccagagcagacagacaaatgaatttcctcagtcacagagtttccagcatatcg 60

QY 61 gatttctggaacagccataatgttcagttcagcccatctactgaacttctgtgaa 120
 Db 61 gatttctggaacagccataatgttcagttcagcccatctactgaacttctgtgaa 120

QY 121 ccatcagaagatgtgagcaaaacaaagattgagattagcattgactgtatccgacgag 180
 Db 121 ccatcagaagatgtgagcaaaacaaagattgagattagcattgactgtatccgacgag 180

QY 181 gactcgacctgagtgaccccaatgtgccaagttacagcaacttggtggtccctgaacagc 240
 Db 181 gactcgacctgagtgaccccaatgtgccaagttacagcaacttggtggtccctgaacagc 240

QY 241 atgaccagcagattcagaacaggtcctcgttccacacagtcctcataacagacacagcg 300
 Db 241 atgaccagcagattcagaacaggtcctcgttccacacagtcctcataacagacacagcg 300

QY 301 cagaacagcgttcacgagccctcgtccctacgcaagccacagctccacctcgaatgtctc 360
 Db 301 cagaacagcgttcacgagccctcgtccctacgcaagccacagctccacctcgaatgtctc 360

QY 361 tctccatcaccccgcaatccctcccaaacagcactaccagagcccgacagtttcgacgtg 420
 Db 361 tctccatcaccccgcaatccctcccaaacagcactaccagagcccgacagtttcgacgtg 420

QY 421 tcttcacagcagtcgagacagcccaagtcgccaactgtagcgtatccactgaactgaag 480
 Db 421 tcttcacagcagtcgagacagcccaagtcgccaactgtagcgtatccactgaactgaag 480

QY 481 aaactctactgcgaatattgcaagaacatgcccatacagaatgtagtgaacccacct 540
 Db 481 aaactctactgcgaatattgcaagaacatgcccatacagaatgtagtgaacccacct 540

QY 541 cctcagagagctgtttacgcgcagctcgtgttataaaaaaactagacagcagcgag 600
 Db 541 cctcagagagctgtttacgcgcagctcgtgttataaaaaaactagacagcagcgag 600

QY 601 gtgtgagcgtgtgcccacacatgagctgagcgttaattcaacagagagcagattgccc 660
 Db 601 gtgtgagcgtgtgcccacacatgagctgagcgttaattcaacagagagcagattgccc 660

QY 661 cctcctagtcattgtatcgagtagaggggaacagccatgcccagatgtagaagatccc 720
 Db 661 cctcctagtcattgtatcgagtagaggggaacagccatgcccagatgtagaagatccc 720

QY 721 atcacaggaagacagagtgctgctgtactatgagccaccccaagttgacctgaattc 780
 Db 721 atcacaggaagacagagtgctgctgtactatgagccaccccaagttgacctgaattc 780

QY 781 acgacagctctgtaacattcatggttaacagcagtggtttgagaggaatgaaacgcgcgt 840
 Db 781 acgacagctctgtaacattcatggttaacagcagtggtttgagaggaatgaaacgcgcgt 840

QY 841 ccaatttaactatgttactctggaacacagagatggaagtcctggtgcgaagcgtgc 900
 Db 841 ccaatttaactatgttactctggaacacagagatggaagtcctggtgcgaagcgtgc 900

QY 901 tttagagcccgagtcgtgtgttccagaggaagacagagccgagttgagagtaagatc 960
 Db 901 tttagagcccgagtcgtgtgttccagaggaagacagagccgagttgagagtaagatc 960

QY 961 agaaagcagcaagtttcgagcagtaacaaagacgtgtagtgcagagcccggttctgt 1020
 Db 961 agaaagcagcaagtttcgagcagtaacaaagacgtgtagtgcagagcccggttctgt 1020


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Db 1021 cagaacacatggtatccagatgacatccatccaagaacgaagatccccagatgagaa 1080
Qy 1081 ctgtatacttaccagtgagggcgcgtagactatgaatgctgttgaagaatcaagag 1140
Db 1081 ctgtatacttaccagtgagggcgcgtagactatgaatgctgttgaagaatcaagag 1140
Qy 1141 tccttggaactcatgtagcttctccccaagacaaattggaactgacaggaacagaa 1200
Db 1141 tccttggaactcatgtagcttctccccaagacaaattggaactgacaggaacagaa 1200
Qy 1201 cagcagcagcagccagcacttacttcagaaga 1232
Db 1201 cagcagcagcagccagcacttacttcagaaga 1232

RESULT 6
AAx58572
ID AAx58572 standard; cDNA; 1926 BP.
XX
AC AAx58572;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cell regulatory protein p63, isoform huTAp63 alpha, cDNA.
XX
KW Cell regulatory protein; p63; huTAp63 alpha; TAp63 alpha; human;
KM cancer; tumour suppressor; cell cycle control; apoptosis;
KM cell proliferation; cell differentiation; therapy; ss.
XX
OS Homo sapiens.
XX
PN MO99191357-A2.
XX
PD 22-APR-1999.
XX
PE 02-OCT-1998; 98MO-US21992.
XX
PR 29-MAY-1998; 98US-0087216.
PR 15-OCT-1997; 97US-0062076.
XX
PA (HARD ) HARVARD COLLEGE.
PI
PI McKeon F, Yang A;
XX
DR WPI; 1999-277595/23.
DR P-PSDB; AAY05953.
XX
XX New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
PS
PS Claim 1; Fig 9; 161pp; English.
XX
XX The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC intron-exon organisation is conserved between p73 and p53, and from
CC known exon and intron sizes for these 2 genes, it was possible to
CC identify new members of this gene family using a PCR-based strategy
CC of amplifying 2 exons in a conserved domain and their intervening
CC intron. The human p53 gene was localised to chromosomal position
CC 3q27-29. At least 6 different isoforms exist. Splice variants
CC differing at the C-terminus have been designated as alpha, beta and
CC gamma forms, while p63 members differing in the N-terminus are
CC designated as delta and TA forms, where the delta form lacks the
CC transactivation domain. The present sequence represents a cDNA
CC clone encoding human TAp63 alpha. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. Delta isoforms of p63

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CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in hematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
CC AAx58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.
XX
SQ Sequence 1926 BP; 509 A; 574 C; 444 G; 399 T; 0 other;

Query Match          91.7%; Score 1232; DB 20; Length 1926;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atgtccagagcacacacacaaatgaattctctcagtcacagagtttccacatatctg 60
Db 1 atgtccagagcacacacacacaaatgaattctctcagtcacagagtttccacatatctg 60
Qy 61 gatttctgaaacagccctatagttcagttcagcccatgacttgaaacttctgtgata 120
Db 61 gatttctgaaacagccctatagttcagttcagcccatgacttgaaacttctgtgata 120
Qy 121 ccatacagaagatgtgtgcgacaacaagaattgagattgacatgagctgatacag 180
Db 121 ccatacagaagatgtgtgcgacaacaagaattgagattgacatgagctgatacag 180
Qy 181 gactcgaagcctggaattgaccccatgtgacacagatgacaaacccctggtctctt 240
Db 181 gactcgaagcctggaattgaccccatgtgacacagatgacaaacccctggtctctt 240
Qy 241 atggaacagcagattcagaacggtctctgtccacagtcctctataacacagacag 300
Db 241 atggaacagcagattcagaacggtctctgtccacagtcctctataacacagacag 300
Qy 301 cagaacagcgtcagacggtcctctgcctacagacagcccaagctccacattgactctc 360
Db 301 cagaacagcgtcagacggtcctctgcctacagacagcccaagctccacattgactctc 360
Qy 361 tctccatccagcccatccctcccaacacagcactacacagcccgccagatttgcagtg 420
Db 361 tctccatccagcccatccctcccaacacagcactacacagcccgccagatttgcagtg 420
Qy 421 tctctccagcagtcgagacacgccaagtgcgccaactgagactatccatgaaactga 480
Db 421 tctctccagcagtcgagacacgccaagtgcgccaactgagactatccatgaaactga 480
Qy 481 aaactctactgccaatgcaagaacatgcccacatccagatcaaggtgataccaccact 540
Db 481 aaactctactgccaatgcaagaacatgcccacatccagatcaaggtgataccaccact 540
Qy 541 cctcagagagctgtatccgcgcacatgctgtctcaaaaagctgacacagtcagag 600
Db 541 cctcagagagctgtatccgcgcacatgctgtctcaaaaagctgacacagtcagag 600
Qy 601 gtgtgaaagcgtgcccacaacatgactgagcgtgtaattcaacagagacagattgccc 660
Db 601 gtgtgaaagcgtgcccacaacatgactgagcgtgtaattcaacagagagacagattgccc 660
Qy 661 cctctagatcttggattcaggtgagggagacagccatgcccagatgataagaattccc 720
Db 661 cctctagatcttggattcaggtgagggagacagccatgcccagatgataagaattccc 720
Qy 721 atccagaagaacagagatgtctgttacctatgagccaccaggttgcagtaattc 780
Db 721 atccagaagaacagagatgtctgttacctatgagccaccaggttgcagtaattc 780
Qy 781 acgacagctctgtacaatttcatgtgtacaagcagttgtgtgagggatgaaccgcgt 840
Db 781 acgacagctctgtacaatttcatgtgtacaagcagttgtgtgagggatgaaccgcgt 840
Qy 841 ccaatttcaatcatgttaccctcgtgaaacacagagatggtgcaagtctcgtgagcgcgtgc 900

```

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Db      841 ccaatttaattcattgttactctggaacacagatgagcgaatccttggccgacgtgc
Qy      901 tttagagccggatctgtgtcttgcgaagaagacagaaagcgatgaagatagatc
Db      901 tttagagccggatctgtgtcttgcgaagaagacagaaagcgatgaagatagatc
Qy      961 agaaagcagcaatcttcgagcaatacaagaacggtgagtgaggaagcccggttgc
Db      961 agaaagcagcaatcttcgagcaatacaagaacggtgagtgaggaagcccggttgc
Qy      1021 cagaacacacatgtatccagatgacatccatcaagaagaatcccccagatgaa
Db      1021 cagaacacacatgtatccagatgacatccatcaagaagaatcccccagatgaa
Qy      1081 cgttatacttaacagtgagggcgctgagacttgaatgctgttgaagatcaaaag
Db      1081 cgttatacttaacagtgagggcgctgagacttgaatgctgttgaagatcaaaag
Qy      1141 tccctggaactatgacgtaactcttcacgacacaaattgaacgttacagcaacagca
Db      1141 tccctggaactatgacgtaactcttcacgacacaaattgaacgttacagcaacagca
Qy      1201 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc
Db      1201 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc

```

RESULT 7
AA25771
ID AA25771 standard; cDNA; 2270 BP.

AC AA25771;

DT 07-JAN-2000 (first entry)

DE Human p51 encoding CDNA B.

KW Human: p51; p53 related gene; cell proliferation; regulation; cancer;
tumour suppression; diagnosis; ss.

OS Homo sapiens.

Key Location/Qualifiers
CDS 145..2070
/*tag- a

W09950412-A1.

PD 07-OCT-1999.

PF 24-MAR-1999; 99MO-JP01512.

PR 27-MAR-1998; 98JP-0100467.

PA (SAKA) OTSUKA PHARM CO LTD.
(IKAWA/) IKAWA Y.

PI Ikawa Y, Ikawa S, Obinata M;

DR WPI: 1999-591318/50.
P-PSDB: AAY45247.

PT New p53 related human gene p51, useful for diagnosis, investigation and
treatment of cancers and screening for potential cell proliferation
agents

Example 1: Page 154-156; 163pp; Japanese.

The present sequence represents a human p51 gene, which is related to
p53 and has cell proliferation regulation and tumour suppression
activity. The p51 gene can be used in the investigation, diagnosis and
treatment of diseases such as cancer, with which the p53 family cell

CC proliferation regulation is associated. The p51 protein may be used for
CC screening potential agonists and antagonists of its regulatory function,
CC for use as drugs,
XX
SQ Sequence 2270 BP; 595 A; 677 C; 500 G; 498 T; 0 other;

Query Match 91.7%; Score 1232; DB 20; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1232; Conservative 0;

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Qy      1 atgtccagagcacaacagacaatgaattcctcagtcagcagagtttcagcatctcg
Db      145 atgtccagagcacaacagacaatgaattcctcagtcagcagagtttcagcatctcg
Qy      61 gatttctggaacagcctatgttcaagttaacggttcacattgacttgaatttgaatga
Db      205 gatttctggaacagcctatgttcaagttaacggttcacattgacttgaatttgaatga
Qy      121 ccatcagaagatggtgagcaacaacagatgagatgaatgactgactgacatcgacg
Db      265 ccatcagaagatggtgagcaacaacagatgagatgaatgactgactgacatcgacg
Qy      181 gactcgacactgagtgaccccatgtgcccacagatcacgaacttgggctcctgaacagc
Db      325 gactcgacactgagtgaccccatgtgcccacagatcacgaacttgggctcctgaacagc
Qy      241 atggaacagcagatcaagaacgctcctcgtccacagtcctctataacagacacagcg
Db      385 atggaacagcagatcaagaacgctcctcgtccacagtcctctataacagacacagcg
Qy      301 cagaacagcgtcaagcgccctcgtccacagtcctcagcaacagcctcagatgactc
Db      445 cagaacagcgtcaagcgccctcgtccacagtcctcagcaacagcctcagatgactc
Qy      361 tctcatcacccgcgcacatccctcacaacagcagatcccatcaacagcagatcttcagctg
Db      505 tctcatcacccgcgcacatccctcacaacagcagatcccatcaacagcagatcttcagctg
Qy      421 tctctcagcagctgagacacgcagtcgacacctcgtgacgtatctccatctgaactga
Db      565 tctctcagcagctgagacacgcagtcgacacctcgtgacgtatctccatctgaactga
Qy      481 aaactctactgccaattgcaagaacatgccccatccatcaagatgagtgacccacact
Db      625 aaactctactgccaattgcaagaacatgccccatccatcaagatgagtgacccacact
Qy      541 cctcagagagctgttatccgctgacatgctgtctacaaaagaacgtgacagcagcagag
Db      685 cctcagagagctgttatccgctgacatgctgtctacaaaagaacgtgacagcagcagag
Qy      601 gtggtgaagcgtgcccccaacatgagctgagccgtgaaatcaacgaaggagacagatgac
Db      745 gtggtgaagcgtgcccccaacatgagctgagccgtgaaatcaacgaaggagacagatgac
Qy      661 cctcctagtcatttgatctgagtagaggggaacagcagatgcccagatgtagaagatccc
Db      805 cctcctagtcatttgatctgagtagaggggaacagcagatgcccagatgtagaagatccc
Qy      721 atcaacagaagacagatgtgctgtaacttatgagcaccacccaggttggacatgaatc
Db      865 atcaacagaagacagatgtgctgtaacttatgagcaccacccaggttggacatgaatc
Qy      781 acgacagctctgtaacatctcatgtgtaacacagctgtgtgtgagagatgaacgcgcgt
Db      925 acgacagctctgtaacatctcatgtgtaacacagctgtgtgtgagagatgaacgcgcgt
Qy      841 ccaatttaacatctgtaacatctgtaacacagatggtgcaagtctggtgcgacgctgc
Db      985 ccaatttaacatctgtaacatctgtaacacagatggtgcaagtctggtgcgacgctgc
Qy      901 tttagagccggatctgtgtcttgcgaagaagacagaaagcggtgagatgaagatagatc

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Db 1045 tttagagccgagatctgtcttgccagagagacaggaagcgagatgaatagatc 1104
QY 961 agaaagcagcaagttctgcagcagtaacaagaacggtgtagtgcagagccgcttcgt 1020
Db 1105 agaaagcagcaagttctgcagcagtaacaagaacggtgtagtgcagagccgcttcgt 1164
QY 1021 cagaacacatgtgtacacagatgacatccatcacagaacagaaatccccagatgagaa 1080
Db 1165 cagaacacacatgtgtacacagatgacatccatcacagaacagaaatccccagatgagaa 1224
QY 1081 ctgttactactacagtgagggcggtgagactatgaaatgtctgttgaagatcaagag 1140
Db 1225 ctgttactactacagtgagggcggtgagactatgaaatgtctgttgaagatcaagag 1284
QY 1141 tcccttgaaactatgcagtaacctctccacagacacaatgtaaacgtacaggaacagaa 1200
Db 1285 tcccttgaaactatgcagtaacctctccacagacacaatgtaaacgtacaggaacagaa 1344
QY 1201 cagcagcagcagcagcagcactactacagaaca 1232
Db 1345 cagcagcagcagcagcagcactactacagaaca 1376

RESULT 8

AAC66028.

ID AAC66028 standard; cDNA; 2270 BP.

XX AAC66028;

DT 21-FEB-2001 (first entry)

DE Human lung cancer-associated cDNA p63 isoform 2.

KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW vaccine; detection; ss.

XX Homo sapiens.

XX MO200061612-A2.

XX PD 19-OCT-2000.

XX PF 03-APR-2000; 2000MO-US08896.

XX PR 02-APR-1999; 9905-0285479.

XX PR 17-DEC-1999; 9905-0466396.

XX PR 30-DEC-1999; 9905-0476496.

XX PR 10-JAN-2000; 2000US-0480884.

XX PR 22-FEB-2000; 2000US-0510376.

XX (CORI-) CORIXA CORP.

XX Wang T, Fan L;

XX MPI: 2000-628399/60.

XX P-PSDB; AAB11358.

XX Isolated polypeptide comprising an immunogenic portion of a lung tumor

XX protein is used for detecting and monitoring progression of lung cancer

XX in a patient -

XX Claim 25a; Page 237-238; 261pp; English.

XX This invention describes a novel isolated polypeptide (I) which

XX comprising an immunogenic portion of a lung tumor protein or variant (P2)

XX CC which have cytostatic activity. The polypeptides and polynucleotides are

XX CC used in compositions and vaccines to inhibit the development of cancer,

XX CC especially lung cancer, in a patient. Methods described in the invention

XX CC can be used to monitor the progression of a cancer by carrying out the

XX CC detection at subsequent time points and comparing the results from the

XX CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient

XX CC are treated with P2, polynucleotides encoding P2 or antigen presenting

XX CC cells expressing P2 and then administered to the patient to inhibit

CC development of cancer.

XX Sequence 2270 BP; 595 A; 676 C; 501 G; 498 T; 0 other;

XX Query Match 91.7%; Score 1232; DB 21; Length 2270;

XX Best local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

XX Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtccagagacacagacaaatgaattcccaagtcagagagtttcagatattcg 60
Db 145 atgtccagagacacagacaaatgaattcccaagtcagagagtttcagatattcg 204
QY 61 gatttttggaacagcctatatgttcagtttcagccatttacttgaacttttgagatga 120
Db 205 gatttttggaacagcctatatgttcagtttcagccatttacttgaacttttgagatga 264
QY 121 ccatcagaagatgtgagcaaaacaaagattgagattgagatgagctgtatccgcatgag 180
Db 265 ccatcagaagatgtgagcaaaacaaagattgagattgagatgagctgtatccgcatgag 324
QY 181 gactcgagaccctgagtgaccccatgtgccaagttacacagaacctggggctctgaacagc 240
Db 325 gactcgagaccctgagtgaccccatgtgccaagttacacagaacctggggctctgaacagc 384
QY 241 atgagcagcagagattcagaacgctcctgttccaacagtcctcataacacagaccagc 300
Db 385 atgagcagcagagattcagaacgctcctgttccaacagtcctcataacacagaccagc 444
QY 301 cagaacagcgttaacgagcctcctgccttagcacaagccagccctccacttcgattgctc 360
Db 445 cagaacagcgttaacgagcctcctgccttagcacaagccagccctccacttcgattgctc 504
QY 361 tctccatcacccgcacatccctcccaacacagactacccaagcccgacagtttcagactg 420
Db 505 tctccatcacccgcacatccctcccaacacagactacccaagcccgacagtttcagactg 564
QY 421 tccctccagcagtcagagaccgccaagtcggccaacttgacgtattccactgaactgaag 480
Db 565 tccctccagcagtcagagaccgccaagtcggccaacttgacgtattccactgaactgaag 624
QY 481 aaactctactgcgaatattgaaagacatgcccatacgaattgaagtgagaccacccct 540
Db 625 aaactctactgcgaatattgaaagacatgcccatacgaattgaagtgagaccacccct 684
QY 541 cctcagggagcgtgtatccgcgcagcatgctgtctacaaaaaagctggacagctcacggag 600
Db 685 cctcagggagcgtgtatccgcgcagcatgctgtctacaaaaaagctggacagctcacggag 744
QY 601 gtgtgtgaagcgtgtgcccacacatgagctgagccgtgaattcaacagagagagattgcc 660
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QY 661 cctcctgattcattgtatgtagtagaggggaacagccattgcccagattgtagaagatccc 720
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QY 721 atcaaggaagacagagtgctgctgtacattatgagccaccaggttgcgactgaattc 780
Db 865 atcaaggaagacagagtgctgctgtacattatgagccaccaggttgcgactgaattc 924
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QY 901 tttagagcccgagatctgtctgtccaggaagacagcaggaagcggatgagatagatc 960
Db 1045 tttagagcccgagatctgtctgtccaggaagacagcaggaagcggatgagatagatc 1104

QY 961 agaaagcagcagcttcgcagcagctacaaagcgtgctgctacgaagcgcgcgttcgt 1020
 Db 1105 agaaagcagcagcttcgcagcagctacaaagcgtgctgctacgaagcgcgcgttcgt 1164
 QY 1021 cagaacacacatggtatccagatgacatccatcaagaacgcagatcccccagatgaa 1080
 Db 1165 cagaacacacatggtatccagatgacatccatcaagaacgcagatcccccagatgaa 1224
 QY 1081 ctgttactactacagtgaggcgctgagactatgtaatgctgttgaagaatcaagag 1140
 Db 1225 ctgttactactacagtgaggcgctgagactatgtaatgctgttgaagaatcaagag 1284
 QY 1141 tcccttgaaactatgcagtaaccttcctcagcacaacatgtaagcgtacaggaacgaa 1200
 Db 1285 tcccttgaaactatgcagtaaccttcctcagcacaacatgtaagcgtacaggaacgaa 1344
 QY 1201 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1232
 Db 1345 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1376

RESULT 9

AAZ43913 standard; cDNA; 4846 BP.

ID AAZ43913

AC AAZ43913

DT 14-MAR-2000 (first entry)

XX Human KET cDNA.

XX KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;

XX p53 family; angiogenic; cytotoxic; cancer; human; ss.

OS Homo sapiens.

XX WO961610-A2.

XX 02-DEC-1999.

XX 25-MAY-1999; 99WO-DE01557.

XX 25-MAY-1998; 98DE-1022985.

(FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX Paul D, Augustin M, Schmale H, Bamberger C;

DR MPI; 2000-063710/05.

XX P-PSDB; MAY50997.

XX New KET-encoding nucleic acid and related proteins, for diagnosis and

XX treatment of tumors -

XX Claim 3; Page 23-26; 28pp; German.

XX This invention describes a novel KET-encoding nucleic acid (I) and its
 CC fragments, variants and mutants which has anticancer activity. (I)
 CC encodes a protein, (II), involved in control of the cell cycle and
 CC apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the
 CC p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to
 CC detect (I) in biological samples, specifically angiogenic tumor tissue,
 CC including (I) sequences that have a homozygotic deletion and (b) to
 CC detect presence or absence of human chromosome 3q27 or murine chromosome
 CC 16, or their fragments, by hybridization. Also, (II) is used as a tumor
 CC suppressor, particularly in tumors where an alteration in the wild-type
 CC p53 allele has not been identified. (I) and (II) may also be used for
 CC development of specific cytotoxic agents and for predicting the risk of
 CC developing cancer. This sequence represents the human KET cDNA sequence
 CC described in the method of the invention.

XX Sequence 4846 BP; 1372 A; 1077 C; 990 G; 1406 T; 1 other;

Query Match 91.7%; Score 1232; DB 21; Length 4846;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtccagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 60
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 QY 61 gatttcggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 120
 Db 205 gatttcggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 264
 QY 121 ccacacagaagatggtgagcagaacagatgagatgagatgagatgagatgagatgagatgag 180
 Db 265 ccacacagaagatggtgagcagaacagatgagatgagatgagatgagatgagatgagatgag 324
 QY 181 gactcgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
 Db 325 gactcgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 384
 QY 241 atgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
 Db 385 atgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 444
 QY 301 cagaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
 Db 445 cagaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 504
 QY 361 tctcacaacccgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 564
 Db 505 tctcacaacccgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 624
 QY 421 tcccttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
 Db 565 tcccttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 624
 QY 481 aaactctactgccaatctgcaagaacatgcccacatcagatcaagtgatgagccacact 540
 Db 625 aaactctactgccaatctgcaagaacatgcccacatcagatcaagtgatgagccacact 604
 QY 541 cctcagagagcgtgtatccgcgcagcagcagcagcagcagcagcagcagcagcagcagcagc 684
 Db 685 cctcagagagcgtgtatccgcgcagcagcagcagcagcagcagcagcagcagcagcagcagc 744
 QY 601 gtgtgagagcgtgtgtcccaacacatgagctgagcgtgtaattcaacagagagcagatgac 660
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 Db 865 atcaacagagagcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 924
 QY 781 acgacagctctgtacaattcatatgttaacagcagcagcagcagcagcagcagcagcagcagc 840
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 Db 1045 tttagagcccgatctgtgcttccagagagagagagagagagagagagagagagagagagagc 1104
 QY 961 agaaagcagcagcttcgcagcagctacaaagcgtgctgctacgaagcgcgcgttcgt 1020
 Db 1105 agaaagcagcagcttcgcagcagctacaaagcgtgctgctacgaagcgcgcgttcgt 1164

[illegible]

| | Best Local Similarity | 100.0%; | Pred. No. 0; | |
|----|-----------------------|---|---------------|-----------|
| | Matches 1232; | Conservative 0; | Mismatches 0; | Indels 0; |
| | | | | Gaps 0; |
| QY | 1 | atgtccagagagacacagacaacaaatgaaatctctcagttccagagagtttccagacatactgg | 60 | |
| Db | 145 | atgtccagagagacacagacaacaaatgaaatctctcagttccagagagtttccagacatactgg | 204 | |
| QY | 61 | gattctctggaacagacctatatgttccagttccagcccatgtgacttgaactttgtgataaa | 120 | |
| Db | 205 | gatttctctggaacagacctatatgttccagttccagcccatgtgacttgaactttgtgataaa | 264 | |
| QY | 121 | ccataagaagatggtgtgcgaacaaagaagtttgatgttaagatgactgtatctccgacatgag | 180 | |
| Db | 265 | ccataagaagatggtgtgcgaacaaagaagatgttaagatgactgtatctccgacatgag | 324 | |
| QY | 181 | gactcgagacttgatgtaaccccatctgtgtgcacacagtaacacgaacacttgggtctcttgaaacagc | 240 | |
| Db | 325 | gactcgagacttgatgtaaccccatctgtgtgcacacagtaacacgaacacttgggtctcttgaaacagc | 384 | |
| QY | 241 | atggaacagcagatctcaagaacggtctctctgtccacacagtcctctataacacagacacgag | 300 | |
| Db | 385 | atggaacagcagatctcaagaacggtctctctgtccacacagtcctctataacacagacacgag | 444 | |
| QY | 301 | cagaaacagcgtatcagcgcgcctcgcgcctctagacacagcccaagttccacctgtatctctc | 360 | |
| Db | 445 | cagaaacagcgtatcagcgcgcctcgcgcctctagacacagcccaagttccacctgtatctctc | 504 | |
| QY | 361 | tctccatcaccccgccatctccctcccaacacacgactacccacagcgccgcacagttctgcagctg | 420 | |
| Db | 505 | tctccatcaccccgccatctccctcccaacacacgactacccacagcgccgcacagttctgcagctg | 564 | |
| QY | 421 | tctcttcacagcagtcgagacacccgacagttcgcacacttgcagtgatltccactgaactgaag | 480 | |
| Db | 565 | tctcttcacagcagtcgagacacccgacagttcgcacacttgcagtgatltccactgaactgaag | 624 | |
| QY | 481 | aaactctactgtcccaattgtcaagagcattgcccacatccagataaagaagtgtatggccccact | 540 | |
| Db | 625 | aaactctactgtcccaattgtcaagagcattgcccacatccagataaagaagtgtatggccccact | 684 | |
| QY | 541 | ccctcagggagcgtctatccgcgcacatgcccctgtctctacaaaanaagcgtgagacgtctcacggag | 600 | |
| Db | 685 | ccctcagggagcgtctatccgcgcacatgcccctgtctctacaaaanaagcgtgagacgtctcacggag | 744 | |
| QY | 601 | gtgtgtgaagcgggtgcccccaacccaatgagctgtgaacggtgaaatctcaacgagggacagatggcc | 660 | |
| Db | 745 | gtgtgtgaagcgggtgcccccaacccaatgagctgtgaacggtgaaatctcaacgagggacagatggcc | 804 | |
| QY | 661 | ccctctagtcatcttattccgagtaagtgaggggaacacagatgcacatgtgccaatatgtataaataccc | 720 | |
| Db | 805 | ccctctagtcatcttattccgagtaagtgaggggaacacagatgcacatgtgccaatatgtataaataccc | 864 | |
| QY | 721 | atccacagagaaacagagtgctgtgtlaaccttatggagcccccaggtttgcactgaatctc | 780 | |
| Db | 865 | atccacagagaaacagagtgctgtgtlaaccttatggagcccccaggtttgcactgaatctc | 924 | |
| QY | 781 | acgacagctctcttaacattctcatgtgtlaacagcagttgttctgtgagggatgtgaacggccgt | 840 | |
| Db | 925 | acgacagctctcttatacaattctcatgtgtlaacagcagttgttctgtgagggatgtgaacggccgt | 984 | |
| QY | 841 | ccaattttaaatactgttaactctgtgaaacacagagatgggcaagttccctgggccgacgcttgc | 900 | |
| Db | 985 | ccaattttaaatactgttaactctgtgaaacacagagatgggcaagttccctgggccgacgcttgc | 1044 | |
| QY | 901 | tttgggccccggaatctgtgtgtcttgcgccaggaagaaagacaggaagcggatgaaataagatc | 960 | |
| Db | 1045 | tttgggccccggaatctgtgtgtcttgcgccaggaagaaagacaggaagcggatgaaataagatc | 1104 | |
| QY | 961 | agaaagcagcagagttcttgagacgtatacaagaacggtgtgatgtatcgaagcggccggttctgt | 1020 | |
| Db | 1105 | agaaagcagcagagttcttgagacgtatacaagaacggtgtgatgtatcgaagcggccggttctgt | 1164 | |
| QY | 1021 | cagaaacacacatgtatccagaatgaacatccatccatcaagaaacgaagaatccccagatgtatgaa | 1080 | |

| | | | |
|----|------|--|------|
| Db | 1165 | cagaacacacactggtatccagatgacatccatcaagaagaagatcccagatgatga | 1222 |
| Qy | 1081 | ctgtatactattaccagtgagagggccgagacttaagaatgctgtttgaagtcagaag | 1140 |
| Db | 1225 | ctgtatactattaccagtgagagggccgagacttaagaatgctgtttgaagtcagaag | 1284 |
| Qy | 1141 | tcctctggaacactgacgtactcctctccagcacacaattgaacgctacaggcaacagca | 1200 |
| Db | 1285 | tcctctggaacactgacgtactcctctccagcacacaattgaacgctacaggcaacagca | 1344 |
| Qy | 1201 | cagcagcagcaccagcacttacttcgaaga | 1232 |
| Db | 1345 | cagcagcagcaccagcacttacttcgaaga | 1376 |

CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC processes. p63 polypeptides (see AA05953-64), polynucleotides (see
CC AA85872-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.

50 Sequence 1182 BP; 330 A; 342 C; 276 G; 234 T; 0 other.

| | | | | |
|----------------------------|--------|----------------|-----------|--------------|
| Query Match | 84.9%; | Score 1140.6; | DB 20; | Length 1182; |
| Best Local Similarity | 98.4%; | Pred. No. 0; | | |
| Matches 1152; Conservative | 0; | Mismatches 19. | Indels 0. | Gap 0. |

| | | | |
|----|------|--|------|
| QY | 174 | aaatgacagagatcccgacctgagtgaaaccatgtggtccacagtaacaagaacctgggtgctct | 233 |
| Db | 9 | ccctggaaatacaatactcccgagatccatttaagttagacacagttatacgaatacctgggtgctct | 68 |
| QY | 234 | gaacacgacatgagaccagcagatctcaagaacggctctctgtccacacagttccctataacaaga | 293 |
| Db | 69 | gaacacgacatgagaccagcagatctcaagaacggctctctgtccacacagttccctataacaaga | 128 |
| QY | 294 | ccaagcgcgagaagaacggttcaacgycgacctgtccctacacgaacagccagatccaccttga | 353 |
| Db | 129 | ccaagcgcgagaagaacggttcaacgycgacctgtccctacacgaacagccagatccaccttga | 188 |
| QY | 354 | tgactctctccacacacccgcgcatcccccctccaaacacagactccacagcgcgcagattt | 413 |
| Db | 189 | tgactctctccacacacccgcgcatcccccctccaaacacagactccacagcgcgcagattt | 248 |
| QY | 414 | cgagcgtctcttcacagcagttcgagacacgcgcgaagtctgagccactctggaagtattccactga | 473 |
| Db | 249 | cgagcgtctcttcacagcagttcgagacacgcgcgaagtctgagccactctggaagtattccactga | 308 |
| QY | 474 | actggaagaanaactctatctgcacaattctgcaagaagacatgccccctccagatccaagttcgatgac | 533 |
| Db | 309 | actggaagaanaactctatctgcacaattctgcaagaagacatgccccctccagatccaagttcgatgac | 368 |
| QY | 534 | ccccactctcttcagggggggcgtgtattccgcgcgaatgctgtctacaaaagaactgtagccagt | 593 |
| Db | 369 | ccccactctcttcagggggggcgtgtattccgcgcgaatgctgtctacaaaagaactgtagccagt | 428 |
| QY | 594 | caacggaagtgtgtgaagcgcgtgtcccaacaacatgagctgaacccgtgaatttcaacaaggagaca | 653 |
| Db | 429 | caacggaagtgtgtgaagcgcgtgtcccaacaacatgagctgaacccgtgaatttcaacaaggagaca | 488 |
| QY | 654 | gaattgccccctccatgaatttgattcgatcgagtgaaggaggacaacatgcccagattgtaga | 713 |
| Db | 489 | gaattgccccctccatgaatttgattcgatcgagtgaaggaggacaacatgcccagattgtaga | 548 |
| QY | 714 | agatcccatcaacagagaagaacagagtgtgtcgtgtacctatgtagccacccccaggtttgccc | 773 |
| Db | 549 | agatcccatcaacagagaagaacagagtgtgtcgtgtacctatgtagccacccccaggtttgccc | 608 |
| QY | 774 | tgaattccacgcagttctgtgtacaatttcattcattgtgtgaacagcagttgtgtctggaaggatga | 833 |
| Db | 609 | tgaattccacgcagttctgtgtacaatttcattcattgtgtgaacagcagttgtgtctggaaggatga | 668 |
| QY | 834 | ccgcgcgtccaattttaattcattgttactctcgtgaacacagagatgggcgaagttctcttgcgcg | 893 |
| Db | 669 | ccgcgcgtccaattttaattcattgttactctcgtgaacacagagatgggcgaagttctcttgcgcg | 728 |
| QY | 894 | -acgctgtcttgaagcccgcgagttcgttctgcccacagagaagaacaggaagcggatgtgaaga | 953 |
| Db | 729 | -acgctgtcttgaagcccgcgagttcgttctgcccacagagaagaacaggaagcggatgtgaaga | 788 |
| QY | 954 | tagcatcagaagaacagcaagttctcgtgacagtaacaagaacgtgtgtgttaagaagcggcc | 1013 |
| Db | 789 | tagcatcagaagaacagcaagttctcgtgacagtaacaagaacgtgtgtgttaagaagcggcc | 848 |
| QY | 1014 | gtttcgtccaaataacacatggtatccagttgacatccatcaagaagaacgagatccccaga | 1073 |

| Query | Match | Best Local Similarity | 83.3% | Score 1119.8 | DB 20 | Length 1452 |
|--------------|---|-----------------------|----------------|--------------|-------|-------------|
| Matches 1212 | Conservative | 0 | Mismatches 120 | Indels 12 | Gaps | |
| QY | 1 atgtccagagacacacagacaatgatctccctcagctccagaggtttccagacatctgg | 60 | | | | |
| DB | 118 atgtccagagacacacagacaatgatctccctcagctccagaggtttccagacatctgg | 177 | | | | |
| QY | 61 gatttctggaacagcctatagtctcaagttccagccatgtgaacttctgtgatgaa | 120 | | | | |
| DB | 178 gatttctggaacagcctatagtctcaagttccagccatgtgaacttctgtgatgaa | 237 | | | | |
| QY | 121 ccatcagaagatggtgagcacaagaattgagattagatgagctgtatccgacatgag | 180 | | | | |
| DB | 238 ccttcgcaaaatggtgagcacaagaattgagattagatgagctgtatccgacatgaa | 297 | | | | |
| QY | 181 gactcgagccttagtgagacccaatgtgagcacaagatcaacgaactctgggctctgaacagc | 240 | | | | |
| DB | 288 gactcgagccttagtgagacccaatgtgagcacaagatcaacgaactctgggctctgaacagc | 357 | | | | |
| QY | 241 atgagccagcagatcagaaagcgctcctcgtccacagctccctataacacagacacagcg | 300 | | | | |
| DB | 358 atgagccagcagatcagaaagcgctcctcgtccacagctccctataacacagacacagca | 417 | | | | |
| QY | 301 cagaacacgctacagcgccctcgcctcgaagacagcagccaggtccacacttgatgtctc | 360 | | | | |
| DB | 418 cagaatagcgttagcgccctcgcctcgaagacagcagccaggtccacacttgatgtctc | 477 | | | | |
| QY | 361 tctcatcacccgcacatccctcccaaacacagctaacccagcgccgacaggtttcgatg | 420 | | | | |
| DB | 478 tctcatcacccgcacatccctcccaaacacagctaacccagcgccgacacagctttgatg | 537 | | | | |
| QY | 421 tctcttcagcagctcgagacagcgccaagctcgagcacttgagcgttatccactgaactgaag | 480 | | | | |
| DB | 538 tctcttcagcagctcgagacacatgcaagctcgagcacttgagcgttatccactgaactgaag | 597 | | | | |
| QY | 481 aaactctatcgcacaaatgacaaagacatgcccacatccagatcaaatgattgacccacact | 540 | | | | |
| DB | 598 aaactctatcgcacaaatgacaaagacatgcccacatccagatcaaatgattgacccacaccc | 657 | | | | |


```
OY 241 atgacacagatctcagaagcgtctctgtccaccagttccctataacacagacagcg 300
DB 358 atgaccacagatctcagaagcgtctctgtccaccagttccctataacacagacagcg 417
OY 301 cagaacagctcagcgcgcctcgccttaagcagccacgcctcctcgtatgtctc 360
DB 418 cagaatagctgagcgcgcctcgccttaagcagccacgcctcctcgtatgtctc 477
OY 361 tctcacaacccgcctcctcctcaacacagactaccagcccgagtttcgaagctg 420
DB 478 tctcacaacccgcctcctcctcaacacagactaccagcccgagtttcgaagctg 537
OY 421 tcttcacagcagtcgacacgcgcacagtcgacacagtcgacacagtcgacacag 480
DB 538 tcttcacagcagtcgacacgcgcacagtcgacacagtcgacacagtcgacacag 597
OY 481 aaactctactgcacaatttcgaagacatgccatccagatcaagtgatgacccacgt 540
DB 598 aagctgtactgcacaatttcgaagacatgccatccagatcaagtgatgacccacgt 657
OY 541 cctcagagagctgttaccgcgcgcgtctgtctacacaaaagctgagcagtcagag 600
DB 658 ccaacagagcgtgttaccgcgcgcgtctgtctacacaaaagctgagcagtcagag 717
OY 601 gttgtgaagcgtgtgtcccaacacatgagcgtgagcgtgaaatcaagagagagatg 660
DB 718 gttgtgaagcgtgtgtcccaacacatgagcgtgagcgtgaaatcaagagagatg 777
OY 661 cctccagcagcatttgaatctcagagagagagagagagagagagagagagagag 720
DB 778 cctccagcagcatttgaatctcagagagagagagagagagagagagagagagag 837
OY 721 atcacagagagagagagagagagagagagagagagagagagagagagagagag 780
DB 838 atcacagagagagagagagagagagagagagagagagagagagagagagagag 897
OY 781 agcagcagcgtgtgtgaacatttcagatgagagagagagagagagagagagag 840
DB 898 agcagcagcgtgtgtgaacatttcagatgagagagagagagagagagagagag 957
OY 841 ccaatttaacatctgtactctcgaacacagagatgggagagagagagagagagag 900
DB 958 ccaatttaacatctgtactctcgaacacagagatgggagagagagagagagagag 1017
OY 901 tttagagcccgagatctgtctgtccagagagagagagagagagagagagagag 960
DB 1018 tttagagcccgagatctgtctgtccagagagagagagagagagagagagagag 1077
OY 961 agaaagcagcagatcttcgacagctacacaaagagcgtgagtgagagagagagag 1020
DB 1078 agaaagcagcagatcttcgacagctacacaaagagcgtgagtgagagagagagag 1137
OY 1021 cagaacacacatggtatcagatgacatccatcaagaagagagagagagagagag 1080
DB 1138 cagaacacacatggtatcagatgacatccatcaagaagagagagagagagagag 1197
OY 1081 cgtgtatctactacagtgagagcgtgagagacttgaagatgctgttgaagatcaagag 1140
DB 1198 cgtgtatctactacagtgagagcgtgagagacttgaagatgctgttgaagatcaagag 1257
OY 1141 tccctggaactatctgacagatctcctcagacacacatggaacgtgacagacagca 1200
DB 1258 tcaactggaactatctgacagatctcctcagacacacatggaacgtgacagacagca 1317
OY 1201 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1232
DB 1318 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1349
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RESULT 14
AA227674
ID AA227674 standard; DNA; 2082 BP.
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XX
AC AA227674;
XX
XX 20-DEC-1999 (first entry)
XX
DE Human p40 coding sequence.
XX
XX Human; p40; p53 homologue; oncogene; diagnosis; proliferative disease;
XX anticancer therapeutic identification; cancer; immunogen; neoplasia;
XX Immunodassay reagent; tumour; dysplasia; hyperplasia; therapy; ss.
XX
XX Homo sapiens.
XX
XX MO9950287-A2.
XX
XX 07-OCT-1999.
XX
XX 26-MAR-1999; 99MO-US06657.
XX
XX 27-MAR-1998; 98US-0079736.
XX
XX (UYJO ) UNITV JOHNS HOPKINS.
XX
XX Trink B, Jen J, Ratovitski E, Sidransky D;
XX
XX WPI; 1999-591272/50.
XX
XX P-PSDB; AAY43135.
XX
XX Isolated oncoproteins used to classify and diagnose tumours, and in
XX screens for identifying anticancer agents -
XX
XX Claim 6; Page 58-59; 63pp: English.
XX
XX
XX This sequence encodes the human p40 protein of the invention. p40 (the
XX shortest variant of a new human p53 homologue) is oncogenic and detection
XX of its overexpression (at protein or nucleic acid levels) is used to
XX diagnose and classify cancers or other proliferative diseases. It can
XX also be used to identify agents, potential anticancer therapeutics, that
XX modulates its binding to p53. p40 (or its fragments or fusion proteins)
XX are used as immunogens to raise (or to purify) antibodies. Antibodies are
XX used as immunodassays reagents for detecting overexpression of p40, also
XX therapeutically against tumours. Fragments of the nucleic acid that
XX encode p40 are used for recombinant expression; as probes to quantify p40
XX gene expression or to identify related sequences; also chromosome 3q.
XX Antisense fragments are useful for inhibiting expression of p40, for
XX treatment of neoplasia, dysplasia and hyperplasia.
XX
XX Sequence 2082 BP; 605 A; 493 C; 473 G; 511 T; 0 other;
XX
XX
XX Query Match 76.7%; Score 1031.2; DB 20; Length 2082;
XX Best Local Similarity 95.7%; Pred. No. 4.2e-292;
XX Matches 1060; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
XX
XX 125 cagaagatggtgacaaacagagatgagtagatgacgtatccgatgcagagact 184
DB 395 cagaagatggtgacaaacagagatgagtagatgacgtatccgatgcagagact 454
OY 185 cgaagctgagtgaccccatgtgcccacagctgacagacagctgggctcctgaagacatgg 244
DB 455 atgccagactcaatttagtgagacagctgacagacagctgggctcctgaagacatgg 514
OY 245 accagagattcagaagcgtcctcgtccacagctccctataacacagacagcgcagaga 304
DB 515 accagagattcagaagcgtcctcgtccacagctccctataacacagacagcgcagaga 574
OY 305 acagcgtcagcgcgcctcgccttaagcagacagcagcagcagcagcagcagcagcagc 364
DB 575 acagcgtcagcgcgcctcgccttaagcagacagcagcagcagcagcagcagcagcagc 634
OY 365 catcacccgcacatccctccacacacagcagcagcagcagcagcagcagcagcagcagc 424
DB 635 catcacccgcacatccctccacacacagcagcagcagcagcagcagcagcagcagcagc 694
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QY 425 tccagcagtcgacacccgcaagtcgcccactgagcgtatctccactgaaagaac 484
 DB 695 tccagcagtcgacacccgcaagtcgcccactgagcgtatctccactgaaagaac 484
 QY 485 tctactgccaatctgcaagaacatgcccactccagatcaagtgatgacccactctc 544
 DB 755 tctactgccaatctgcaagaacatgcccactccagatcaagtgatgacccactctc 544
 QY 545 agggagcgttataccgcccactgctgtctataaaaaagctgagcaagtcagaggtg 604
 DB 815 agggagcgttataccgcccactgctgtctataaaaaagctgagcaagtcagaggtg 604
 QY 605 tgaagcggctgcccacacacatgagctgagccgtgaaatcaacggaggaagattgcccc 664
 DB 875 tgaagcggctgcccacacacatgagctgagccgtgaaatcaacggaggaagattgcccc 664
 QY 665 ctatgcatctgagtcgagtagagggaggaacacatgcccagatagtgaagaatcccatca 724
 DB 935 ctatgcatctgagtcgagtagagggaggaacacatgcccagatagtgaagaatcccatca 724
 QY 725 cagggaacacagagtgctgctgtaacctatgagccacccaggttgacatgaatcaaga 784
 DB 995 cagggaacacagagtgctgctgtaacctatgagccacccaggttgacatgaatcaaga 784
 QY 785 cagctctgtacaaatctcatcgtgttaacagagtgctgtgagggatgaacccgctccaa 844
 DB 1055 cagctctgtacaaatctcatcgtgttaacagagtgctgtgagggatgaacccgctccaa 844
 QY 845 tttaatactgttactctggaacacagagatgagcaagctctgagccagagctgcttg 904
 DB 1115 tttaatactgttactctggaacacagagatgagcaagctctgagccagagctgcttg 904
 QY 905 agggccggaatccgctgctgcccaggaagacaggaaggcgagatgaagatagatcaaga 964
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 QY 965 agcagcaagtttcgagcagatcaagaagcgtgtgtgtacgaagcgcgcttcgctca 1024
 DB 1235 agcagcaagtttcgagcagatcaagaagcgtgtgtgtgtacgaagcgcgcttcgctca 1024
 QY 1025 acacacatgcatccagatgacatcaacacaggaacaggaatccacagatgatactg 1084
 DB 1295 acacacatgcatccagatgacatcaacacaggaacaggaatccacagatgatactg 1084
 QY 1085 tatacttaaccagtgagggcgctgagactatgaatgtcgtgtgaaagatcaagaagtc 1144
 DB 1355 tatacttaaccagtgagggcgctgagactatgaatgtcgtgtgaaagatcaagaagtc 1144
 QY 1145 tggaaactatgcatcctctcctcagcacacacatggaacgctacagggcacaagcagc 1204
 DB 1415 tggaaactatgcatcctctcctcagcacacacatggaacgctacagggcacaagcagc 1204
 QY 1205 agcagacccagcactactcagaaga 1232
 DB 1475 agcagacccagcactactcagaaga 1502

RESULT 15
 AAC66030
 ID AAC66030 standard; cDNM: 2082 BP.
 XX
 AC AAC66030;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE Human Lung cancer-associated cDNA p63 isoform 4.
 XX
 KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 XX
 OS vaccine; detection; ss.
 XX
 OS Homo sapiens.

PN W0200061612-A2.
 PD 19-OCT-2000.
 XX
 PF 03-APR-2000; 2000MO-US08896.
 XX
 PR 02-APR-1999; 9905-0285479.
 PR 17-DEC-1999; 9905-0466396.
 PR 30-DEC-1999; 9905-0476496.
 PR 10-JAN-2000; 2000US-0480884.
 PR 22-FEB-2000; 2000US-0510376.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Wang T, Fan L;
 XX
 DR WPI; 2000-628399/60.
 DR P-PSDB; AAB11360.
 XX
 PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 XX in a patient -
 PS Claim 25a; Page 239-240; 261pp; English.
 CC
 CC This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.
 XX
 SQ Sequence 2082 BP; 605 A; 493 C; 473 G; 511 T; 0 other;

Query Match 76.7%; Score 1031.2; DB 21; Length 2082;
 Best Local Similarity 95.7%; Pred No. 4.2e-292;
 Matches 1060; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 125 cagaagaatgctggaacaaacagattgagatgacatgactgataccgcatgaggaact 184
 DB 395 cagaagaagaagaaagacagattgacatcttaacatgatacattgttactgtaaaaca 454
 QY 185 cggacctgagtgaccacatgctgcccagatcaagaacttgggtctcctgaagaactg 244
 DB 455 atgccagactcaattttagtgagccacagtaacacgaacctgggtctcctgaagaactg 244
 QY 245 accagagaattagaagaagctcctctgctacacagatccctataacacagacagcgag 304
 DB 515 accagagaattagaagaagctcctctgctacacagatccctataacacagacagcgag 304
 QY 305 acagcgtacggcgccctcgccctcagacagacagccagctcactccatgactgtctctc 364
 DB 575 acagcgtacggcgccctcgccctcagacagacagccagctcactccatgactgtctctc 364
 QY 365 catcacccgcatccctccacacacagcactaccacagcccgacagtttcgagagtgct 424
 DB 635 catcacccgcatccctccacacacagcactaccacagcccgacagtttcgagagtgct 424
 QY 425 tccagcagtcgagcaccgcaagtcgcccacactgagcagatccatcgaactgaagaac 484
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 QY 485 tctactgccaatctgcaagaacatgcccactccagatcaagtgatgacccactctc 544
 DB 755 tctactgccaatctgcaagaacatgcccactccagatcaagtgatgacccactctc 544
 QY 545 agggagcgttataccgcccactgctgtctataaaaaagctgagcaagtcagaggtg 604

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OY 605 tgaagcgggtgcccaaccaatgagctgagcgttgaattcaacgaggagacagattgccttc 664
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Db 875 tgaagcgggtgcccaaccaatgagctgagcgttgaattcaacgaggagacagattgccttc 934
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OY 665 ctatcttcttctcgtgtagagggaacacatgcccagtagtagaagaatcccatca 724
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Db 935 ctatcttcttctcgtgtagagggaacacatgcccagtagtagaagaatcccatca 994
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|||||
Db 1415 tgaactcatgcaatgacctctcagcacacaatgaaacgtacaggaacagcacagc 1474
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OY 1205 agcagcaacagacttacttcagaaca 1232
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Db 1475 agcagcaacagacttacttcagaaca 1502
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Search completed: August 10, 2001, 00:38:26
Job time: 4025 sec

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QY 482 aactctactgccaatctgcaagaacagatcccatccagatcaagtgatgaacccactc 541
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Db 422 AGATGTTTGGCAACTGCGCAAGACCTGGCTGTGACGCTGTGGTGTATTCACACGCC 481
QY 542 ctcaaggaagtgatattatccgcgcacatgcctgtctacaaaaagctgagcaagtcagag 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 CGCCGGGACACCGCGCTCCGGCCATGCGCATCTTACAAAGCATCAGTCACATGAGGAG 541
QY 602 tggtagaagcggctgcccacacagatgagccggtgaattcaacagaggaacgattgccc 661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 TTGTGAGGCGCTGCCCCACCATGAGCGCTGCTCAGATAGCCATG-----GTCTGGCC 595
QY 662 ctctagtcatttgatctgagtgagaggggaagacacatgcccagatgtagaagatccca 721
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Db 596 CTCCTCAGCATCTTATCCAGTGGAGAAATTTGGTGTGAGTATTTGATGACAGAA 655
QY 722 tcaaggaagacagagtgctgctgagatccctatgagccacccagtgagcaactgaatca 781
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Db 656 ACACCTTTGACATAGTGTGTGATACCTTATGAGCCCGCTGAGGTGCTCTGACTGTATA 715
QY 782 cgacagctctgacaaattcaatgctgaacagcagtgctgttgagaggaatgaacgcgcgtc 841
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 716 CCACCATTCACATCACTACATGATGTAAACAGTTCTGCTGCGGGCGCATGAAACCGAGCC 775
QY 842 caatttaatactatgtactctggaacacagagatggcgaagtcctctgagccgacgtgct 901
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 776 CCATCCTCAGCATCATCACTGGAAGACCTCAGTGGTAACTCTGAGGAGGAAACAGCT 835
QY 902 ttgagcccgagatctgtgctgcccaggaagagacagaggaagcgatgaatgaatgaatca 961
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 836 TTGAGGTGCGTGTGTGCTCTCTGCTGGAGAGACCGCGCAGACAGAGAAAGAAATCTCC 895
QY 962 gaaagcagcaggttctgagcagatcaagaacagtgatgtagaagacgcgcgttctgctc 1021
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 896 GCAAGAAAGGGAGGCTCCACACAGACCTCCCGCAGGAGACACTAAACGAGCACTGCCCCA 955
QY 1022 agaacacacatggtatccagatgacatccatcaagaagaagatcccccagatgataaac 1081
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 956 ACAACAC-----CAGCTCTCTCCCGACGCAAGAAAGAAACACTGTGATGGAGAAAT 1006
QY 1082 tgtatacttaccagtgagggccgtgagactatgaatgctggtgagatcaagaagat 1141
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1007 ATTTCACCCCTCAATCCGGGGGCGTGAAGCTTCCGAATGTTCCGAGAGCTGAATGAGG 1066
QY 1142 cccctggaactcatgagctacatccctcctcagca 1172
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Db 1067 CCTTGAACTCAAGGATGCCAGGCTGGGAA 1097

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST580USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
FAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-431-357-20

Query Match      18.2%  Score 244.2; DB 1; Length 1215;
Best Local Similarity 58.3%  Pred. No. 5.5e-64;
Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

QY 362 ctccacaccgcccacccctcccaaacacgactaccagccgcgacagtttcgagtgat 421
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Db 302 CCTGTGATCTTCTGTCTCTCCCTCCAGAAACCTACACAGGCGAGCTAGCGTTCCGTGTG 361
QY 422 ccttcacagcagtcgagcagccgacgaatcgccacgtgacgtatctccactgaactgaaga 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 GCTTCTTCATCTTGGGAGACGACCAAGCTGTGACTTCACAGTACTCCCTGCCCTCAACA 421
QY 482 aactctactgccaatctgcaagaacagatcccatccagatcaagtgatgaacccactc 541
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Db 422 AGATGTTTGGCAACTGCGCAAGACCTGGCTGTGACGCTGTGGTGTATTCACACGCC 481
QY 542 ctcaaggaagtgatattatccgcgcacatgcctgtctacaaaaagctgagcaagtcagag 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 CGCCGGGACACCGCGCTCCGGCCATGCGCATCTTACAAAGCATCAGTCACATGAGGAG 541
QY 602 tggtagaagcggctgcccacacagatgagccggtgaattcaacagaggaacgattgccc 661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 TTGTGAGGCGCTGCCCCACCATGAGCGCTGCTCAGATAGCCATG-----GTCTGGCC 595
QY 662 ctctagtcatttgatctgagtgagaggggaagacacatgcccagatgtagaagatccca 721
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 596 CTCCTCAGCATCTTATCCAGTGGAGAAATTTGGTGTGAGTATTTGATGACAGAA 655
QY 722 tcaaggaagacagagtgctgctgagatccctatgagccacccagtgagcaactgaatca 781
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 656 ACACCTTTGACATAGTGTGTGATACCTTATGAGCCCGCTGAGGTGCTCTGACTGTATA 715
QY 782 cgacagctctgacaaattcaatgctgaacagcagtgctgttgagaggaatgaacgcgcgtc 841
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 716 CCACCATTCACATCACTACATGATGTAAACAGTTCTGCTGCGGGCGCATGAAACCGAGCC 775
QY 842 caatttaatactatgtactctggaacacagagatggcgaagtcctctgagccgacgtgct 901
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 776 CCATCCTCAGCATCATCACTGGAAGACCTCAGTGGTAACTCTGAGGAGGAAACAGCT 835
QY 902 ttgagcccgagatctgtgctgcccaggaagagacagaggaagcgatgaatgaatgaatca 961
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 836 TTGAGGTGCGTGTGTGCTCTCTGCTGGAGAGACCGCGCAGACAGAGAAAGAAATCTCC 895
QY 962 gaaagcagcaggttctgagcagatcaagaacagtgatgtagaagacgcgcgttctgctc 1021
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Db 896 GCAAGAAAGGGAGGCTCCACACAGACCTCCCGCAGGAGACACTAAACGAGCACTGCCCCA 955

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Query Match 18.2%; Score 244.2; DB 4; Length 1215;
 Best Local Similarity 58.3%; Pred. No. 5.5e-64;
 Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

QY 362 ctccatccaccgcatccctcccaaacaccgagcccgccagcttgcagctg 421
 DB 302 cccctgcatctctctccctcccaaacaccgagcccgccagcttgcagctg 361
 QY 422 ccttccagcagtcgagcccgccagcttgcagcttgcagcttgcagcttgc 361
 DB 362 gctctctgattcttgagcagccagcttgcagcttgcagcttgcagcttgc 421
 QY 482 aactctactgccaattgcaagacatgcccacagatcagcaagtgatgacccac 541
 DB 422 agatgttctgcaacatgagcagccctgctgagctggtggttgcagcttgc 481
 QY 542 ctcaaggagcgtttatccgagccatgcttcttcaaaaagcttgagccgctgag 601
 DB 482 cgcgcgagcagccgctgctgagccagcttctcaagcagctacagcagcagcag 541
 QY 602 tctgagagcgttgcagccacatgagctgagccgctgagcttgcagcttgc 661
 DB 542 tctgagagcgttgcagccacatgagctgagccgctgagcttgcagcttgc 601
 QY 662 ctccatgcttgcagcttgcagcttgcagcttgcagcttgcagcttgcagct 595
 DB 596 ctccatgcttgcagcttgcagcttgcagcttgcagcttgcagcttgcagct 721
 QY 722 tccacaggaagacagagtgctgctgagcttgcagcttgcagcttgcagct 655
 DB 656 acactcttgcagcagtgctgctgagcttgcagcttgcagcttgcagcttgc 715
 QY 782 cgacagcttctgtaacattcagcttgcagcttgcagcttgcagcttgcagct 841
 DB 716 ccacccatccacactacactacatgcttgcagcttgcagcttgcagcttgc 775
 QY 842 caatttaacttcttgcagcttgcagcttgcagcttgcagcttgcagcttgc 901
 DB 776 ccatctctccatccacactacactacatgcttgcagcttgcagcttgcagct 835
 QY 902 tctgagcgcagcttgcagcttgcagcttgcagcttgcagcttgcagcttgc 961
 DB 836 tctgagcgcagcttgcagcttgcagcttgcagcttgcagcttgcagcttgc 895
 QY 962 gaaagcagcagcttgcagcttgcagcttgcagcttgcagcttgcagcttgc 1021
 DB 896 gcaagaaagcagcagcttgcagcttgcagcttgcagcttgcagcttgcagct 955
 QY 1022 agaacacacatgcttgcagcttgcagcttgcagcttgcagcttgcagct 1081
 DB 956 acaacacac-----cagcttctctcccaagcagcagcagcagcagcagc 1006
 QY 1082 tcttacttaccagtgagcgcgtgagcagcttgcagcttgcagcttgcagct 1141
 DB 1007 attcacccttgcagcttgcagcgcgtgagcagcttgcagcttgcagcttgc 1066
 QY 1142 cccctgagcagcagcttgcagcgcgtgagcagcttgcagcgcgtgagcag 1066
 DB 1067 ccttgcagcagcagcttgcagcgcgtgagcagcgcgtgagcagcgcgtgag 1097

RESULT 5
 PCT-US95-15353-20
 ; Sequence 20, Application PC/TUS9515353
 ; GENERAL INFORMATION:
 ; APPLICANT: The Wistar Institute of Anatomy
 ; APPLICANT: and Biology
 ; APPLICANT: Halazonetis, Thanos D.
 ; TITLE OF INVENTION: p53 Proteins With Altered
 ; NUMBER OF INVENTION: Tetramerization Domains
 ; CORRESPONDENCE ADDRESS: 46
 ; ADDRESS: Howson and Howson

STREET: Spring House Corporate Cntr., PO Box 457
 CITY: Spring House
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19477
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/15353
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/347,792
 FILING DATE: 28-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/431,357
 FILING DATE: 28-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/456,623
 FILING DATE: 01-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-540-9206
 TELEFAX: 215-540-5818
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1215 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 PCT-US95-15353-20

Query Match 18.2%; Score 244.2; DB 5; Length 1215;
 Best Local Similarity 58.3%; Pred. No. 5.5e-64;
 Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

QY 362 ctccatccaccgcatccctcccaaacaccgagcccgccagcttgcagctg 421
 DB 302 cccctgcatctctctccctcccaaacaccgagcccgccagcttgcagctg 361
 QY 422 ccttccagcagtcgagcccgccagcttgcagcttgcagcttgcagcttgc 361
 DB 362 gctctctgattcttgagcagccagcttgcagcttgcagcttgcagcttgc 421
 QY 482 aactctactgccaattgcaagacatgcccacagatcagcaagtgatgacccac 541
 DB 422 agatgttctgcaacatgagcagccctgctgagctggtggttgcagcttgc 481
 QY 542 ctcaaggagcgtttatccgagccatgcttcttcaaaaagcttgagccgctgag 601
 DB 482 cgcgcgagcagccgctgctgagccagcttctcaagcagctacagcagcagcag 541
 QY 602 tctgagagcgttgcagccacatgagctgagccgctgagcttgcagcttgc 661
 DB 542 tctgagagcgttgcagccacatgagctgagccgctgagcttgcagcttgc 601
 QY 662 ctccatgcttgcagcttgcagcttgcagcttgcagcttgcagcttgcagct 595
 DB 596 ctccatgcttgcagcttgcagcttgcagcttgcagcttgcagcttgcagct 721
 QY 722 tccacaggaagacagagtgctgctgagcttgcagcttgcagcttgcagct 655
 DB 656 acactcttgcagcagtgctgctgagcttgcagcttgcagcttgcagcttgc 715
 QY 782 cgacagcttctgtaacattcagcttgcagcttgcagcttgcagcttgcagct 841

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Db 716 CCACATCCCTACACACTACATGTGTACAGTCTCTGCATGGCGGCGATCAACCGGAGGC 775
Oy 842 caatttaacatctgtactcttgaaacacagagatgggcaagtcctgggcgcgcgtgct 901
Db 776 CCATCTCACCACATCACTGAGAGACTCCAGTGTATCTACGTGGAGGAGCAAGCT 835
Oy 902 ttgaagcccgatctgtcttgcacaggaagacgaagcgatgataagatca 961
Db 836 TTAGGTGCTGTGTGTGTGCTGTCTGGGAGAGACCGGCCACAGAGAGAAATCTCC 895
Oy 962 gaagagacgaagtttgagagagataaagaagcgatgtagaagagcgcttgc 1021
Db 896 GCAGAGAAAGGGAGCCCTCACACAGAGCTCCCGCAGGAGAGCGAGCACTGCCA 955
Oy 1022 agaacacacatgtatccagatgacatccatcaagaagaagatcccgatgatac 1081
Db 956 ACAGAC-----CAGCTCTCTCCCGACGCAAGAGAAACCACTGTGAGAGAT 1006
Oy 1082 tgttaacttaacagtgagggcgctgagacttaagaatctgttgaagataaagagt 1141
Db 1007 ATTTCACCCCTTCAGATCCGCGGGCGTGAGCGCTTCGAAATGTTCCGAGACTGAATGAG 1066
Oy 1142 ccctggaactcatgacgtactctcccaagca 1172
Db 1067 CCTTGAACCTCAAGAGATGCCAGGCTGGGAA 1097

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RESULT 6
US-08-486-663A-18
; Sequence 18, Application US/08486663A
; Patent No. 5968761
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Eckstein, Jens W.
APPLICANT: Draela, Giulio
APPLICANT: Guillaume Cottarel
TITLE OF INVENTION: Ubiquitin Conjugating Enzymes
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,663A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-029CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

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; NAME/KEY: CDS
; LOCATION: 1..1182
US-08-486-663A-18

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Query Match 18.1%; Score 242.6; DB 2; Length 1181;
Best Local Similarity 58.2%; Pred. No. 1.7e-63;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

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Oy 362 ctccatcaccgcgcacccctcccaacacagcactacccagggccgcagcttgcagctgt 421
Db 275 CCCTGTATCTTGTGTCTCCCTCCAGAAACCTACAGAGGCGACACTACGTTTCCGTCTG 334
Oy 422 ccttcagcaagctgagacacgcgcagctgcgcacctgagacatctccaatgaatgaaga 481
Db 335 GCTTCTTGCATTTCTGGAGACGACCAAGCTGTGTGATCTTCACAGTCTCCCTCCCTCACA 394
Oy 482 aactctactcccaaatgtgcaagaagacatgcccacatccagatccaaggtgatagacccac 541
Db 395 AGATGTTTCCCAACTGCGCCAGACCTGCCCCGTGCGAGCTGTGGGTGATTCACACACCC 454
Oy 542 ctcaggaagctgtatccgcgcacatgctgtctacaacaaagctgagacgttcagagag 601
Db 455 CGCCCGCACCCGCGTCCGCGCATGCGCATGTACAGACGTCACAGCATATGACGAGG 514
Oy 602 tgttgaagcggtgccccacacatgagctgagccggtgaattcaacgagggagacatggccc 661
Db 515 TTGTGAGCGCTCCGCCACCATGAGCGCTGTCAGATGCGATG-----GTCTGGCCC 568
Oy 662 ctccatgacttgcattgcagtagtagagagagacagccatgcccagttgtagaagatccca 721
Db 569 CTCTCTCAGCATCTTATCCAGTGGAGAGAAATTTGCTGTGGAGTATTTGGATGAGAGAA 628
Oy 722 tcacaggaagacagagtgctgtgtacattatgagccacccagttgagacgtgaattca 781
Db 629 ACACTTTTCACATAGTGTGTGTGTGCTGTATGAGCGCGCTGAGTGTGCTGTGACTGTA 688
Oy 782 cgacagctctgtacaattatgtgtacagcagtggtgtgtgagagatgaacgcgcgtc 841
Db 689 CCACATCCACATCACTACATGATGTATGATGATGATGATGATGATGATGATGATGATG 748
Oy 842 caatttaacatctgtactcttgaaacacagagatgggcaagtcctgggcgcgcgtgct 901
Db 749 CCATCTCACCACATCACTACACTGGAAGACTCCAGTGTATTTACTGTGGAGCAACAGCT 808
Oy 902 ttgaagcccgatctgtcttgcacaggaagacagagcgatgataagataagatca 961
Db 809 TTAGGTGCTGTGTGTGTGCTGTCTGGGAGAGACCGGCCACAGAGAGAGATCTCC 868
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Db 869 GCAGAGAAAGGGAGCCCTCACACAGAGCTCCCGCAGGAGACACTAAGCGAGCACTGCCA 928
Oy 1022 agaacacacatgtatccagatgacatccatcaagaagaagaatcccgatgataagac 1081
Db 929 ACAGAC-----CAGCTCTCTCCCGACGCAAGAGAAACCACTGTGATGAGAGAT 979
Oy 1082 tgttaacttaacagtgagggcgctgagacttaagaatctgttgaagataaagagt 1141
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Oy 1142 ccctggaactcatgacgtactctcccaagca 1172
Db 1040 CCTTGAACCTCAAGAGATGCCAGGCTGGGAA 1070

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RESULT 7
US-08-247-904B-11
; Sequence 11, Application US/08247904B
; Patent No. 5981699
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Eckstein, Jens W.

```


Patent No. 5843654
GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
APPLICANT: OLDENBURG, MARY C.
APPLICANT: HEISLER, LAURA
TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSHOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,956
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,601
FILING DATE: 09-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,164
FILING DATE: 09-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL J, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01801
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
TELEFAX: (415) 705-8410
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-956-94

Query Match 18.1%; Score 242.6; DB 2; Length 1182;
Best Local Similarity 58.2%; Pred. No. 1.7e-63;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

QY 362 ctcacatccgcgcacatccctcccaacacgcgacacccagccgcgcacagttcgagcgtgt 421
DB 275 CCTGTGATCTTCTGCTCCCTCCAGAAAACCTACACGAGGACGCTACGGTTCCGCTGTG 334
QY 422 ccttcagagtgtagacacacgaagtgcgcacccctggagcgtatctccatgaactgaaga 481
DB 335 GCTTCTGCTGCTTGTGGACACCAAGCTGTGTGACTTGACAGTACTCCCTGCGCTCAACA 394
QY 482 aactctactgcacaaatgcacaaacacatgcacacacagatcaagtgtagacccacac 541
DB 395 AGATGTTTGGCAACAGCGGCAAGACCTGCGCTGTGACAGCTGTGGGTGATTCCACACCCC 454

QY 542 ctcagagtagctgttatccgcgcacatgcctgtctacaaaaagctgagcagcgtacgag 601
DB 455 CGCCCGGACCCCGCTCCGGCCATGCGCATCTACAGCAGTACACGACATACGCGAG 514
QY 602 tggtagagcgtgtccccaacacatgacgtgagcgtgaattcaacgagggacagattgcc 661
DB 515 TTGTGAGGCGCTGCCCGCCACATGAGGCGTGTGCATGACGATG-----GCTGCGCC 568
QY 662 ctcctagtcattgttagtagagtagagggaaacagcagccacgtatgtagaatccca 721
DB 569 CTCCTGAGCATCTTATCCGATGAGGAAATTTGCTGTGGATATTTCGATGACAGAA 628
QY 722 tcaaggaagacagagtgctgtgaccttaagaccacccagattggacgaattca 781
DB 629 ACACTTTTGCACATGATGTGTGTGCTGTATGAGCGCGCTGAGTGTGCTGTACTGTA 688
QY 782 cgacagctctgtacaaattcatgttaacagcagttgttggaggatgaaccgcgc 841
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QY 842 caatttaacatgttactctgaaacacagatgaggcaagtcctggcgcagcgtgct 901
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QY 902 ttgagcccgatctgtgcttgcggaggaagacaggaagggagatgaagataagcata 961
DB 809 TTGAGGTGCTGTTGTGTGCTGTGGAGAGACCGGCCACAGAGAGAAATCTCC 868
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DB 869 GCAAGAAAGGGAGCCCTACACAGAGCTGCCGCCAGGAGACACTAAGCGACACTGCCCA 928
QY 1022 agaacacacatglatcagatgacatccatcaagaacagagatccacagatgagac 1081
DB 929 ACAACAC-----CAGCTCTCTCCACGCCAAGAAACCACTGATGAGGAAAT 979
QY 1082 tgtatactaccagtagagggccgtgagactatgaatgctgttgaagataaagag 1141
DB 980 ATTTACCCCTTCAGATCCGTGGGGTGAGCGCTTCGAGATGTTCCGAGACTGAATGAGG 1039
QY 1142 ccctggaactatgcagtlaccttcccaaga 1172
DB 1040 CCTTGAACCTCAAGATGCCACAGCTGGAA 1070

RESULT 12
US-08-757-653-92
Sequence 92, Application US/08757653
Patent No. 5843659
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:


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Db 569 CTCCTGACGATCTTATCCGAGTGGAGAAATTTGCTGTGGAGTATTTGATACAGAA 628
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QY 782 cgacagtcctgtacatctatcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 841
Db 689 CCACATCCATCTACACATACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 748
QY 842 caatttaaatcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 901
Db 749 CCATCCCTACACATCATACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 808
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Db 809 TTGAGGTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 868
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RESULT 14

US-08-458-356-215
Sequence 215, Application US/08458356
Patent No. 5942235

GENERAL INFORMATION:

APPLICANT: Paolletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,356
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS

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; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-458-356-215

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Query Match 18.1%; Score 242.6; DB 2; Length 1182;
Best Local Similarity 58.2%; Pred. No. 1.7e-63;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

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Db 335 GCTTCTTGATTCGTGGACACCAAGTCTGTGACTTGACAGTACTCCCTGCTCCTCAACA 394
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Db 455 CGCCCGGACCCCGCGCTCCGCGCATGCGCATCAAGCACTACACACATGACGAGG 514
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Db 515 TTGTAGAGCGCTGCCCCACCATGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 568
QY 662 ctccatcatcttgatctgagtagagggagacagcatalgcccagatgtagaatccca 721
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RESULT 15

US-08-796-101-46

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; Sequence 46, Application US/08796101
; Patent No. 6183752
; GENERAL INFORMATION:
; APPLICANT: EPSTEIN, STEPHEN E.
; APPLICANT: FINKEL, TOREN
; APPLICANT: SPEIR, EDITH
; APPLICANT: ZHOU, YI FU
; APPLICANT: ZHU, JIANHUI
; APPLICANT: ERDLE, LORNE
; APPLICANT: PINCUS, STEVEN
; TITLE OF INVENTION: RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,
; TITLE OF INVENTION: PROPHYLAXIS AND THERAPY
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,101
; FILING DATE: 05-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: KOMALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 764-5574
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-796-101-46

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Query Match      18.1%; Score 242.6; DB 4; Length 1182;
Best Local Similarity 58.2%; Pred. No. 1.7e-63;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

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QY 662 ctccatagcatitgattcagatagaggaagaaacagcattgcccagatgtagaagaatccca 721
DB 569 CTCCTCAGCATCTTATCCAGAGTGAAGAAATTTGCGTGTGAGATATTGATGATGACAGAA 628

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QY 722 tcacaggaagacagagtgctgtgttaccttatgagccaccaggttggacgtgaattca 781
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2001, 23:30:41 ; Search time 1394.72 Seconds
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9109.094 Million cell updates/sec

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Perfect score: 1344
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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 BASE COUNT 147 a 113 c 141 g 113 t
 ORIGIN

Query Match 35.9%; Score 483; DB 115; Length 514;
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 Matches 497; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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 AUTHORS HGP
 TITLE http://www.ludwig.org.br/ORESTES.
 JOURNAL The FAPESP/LICR Human Cancer Genome Project
 COMMENT Unpublished (1999)
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-HT0322-201299-135-e02&t3=1999-12-20&t4=1)
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FEATURES
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 /dev_stage="Adult"
 /note="Organ: head,neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 146 a 123 c 140 g 108 t
 ORIGIN

Query Match 34.7%; Score 467; DB 115; Length 517;
 Best Local Similarity 95.7%; Pred. No. 2.7e-121;
 Matches 506; Conservative 0; Mismatches 10; Indels 13; Gaps 2;

OY 536 caactcctcagagagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 595
 Db 1 caactcctcagagagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 60
 OY 596 cggaggtggtgtagagcggtgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 655
 Db 61 cggaggtggtgtagagcggtgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 120
 OY 656 ttgcctcctcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 715
 Db 121 ttgcctcctcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 180
 OY 716 atccatcaagaagaagaatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 775
 Db 181 atccatcaagaagaagaatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 834
 OY 776 aattcagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 894
 Db 241 aattcagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 954
 OY 895 cgcgtcctttagagcccgatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 954
 Db 361 cgcgtcctttagagcccgatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 420
 OY 955 agcatcagaagaagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagatgtagcagat 1014

Db 421 AGCATGAGAAAGCAGAGTTTGGACAGTACAAAGAACGGTGATG-----CG 468

QY 1015 ttccgtcagaacacacatggtatccagatgacatccatccaagaagaa 1063
|||||
Db 469 TTTGCTGACAGAACACTATGATCCAGATCCATCCATCAAGAACGAA 517

RESULT 7
BF774398 450 bp mRNA EST 12-JAN-2001
LOCUS 284057 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BF774398
ACCESSION BF774398
VERSION BF774398.1 GI:12122298
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 450)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrrentug,S.C., Freking,B.A., Rohrer,G.A., Laegreid,
W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
JOURNAL
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Place: 83 row: C column: 20
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. 450
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT 130 a 122 c 113 g 85 t
ORIGIN

Query Match 30.4%; Score 408.4; DB 169; Length 450;
Best Local Similarity 94.2%; Pred. No. 1e-104;
Matches 424; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 876 tgggcaagctctggcgcaagctgcttggagcccgatctgcttggcgcaagaaaga 935
|||||
Db 1 TGGGCAAGTCTCTGGGCGCGCTGCTTTGAGGCCGCGATCTGCTTGGCCAGGAGAGA 60

QY 936 caggaaagcgagatgaatgacatcagaagaagcagagtttcgacagtlacaagaacg 995
|||||
Db 61 CAGGAAGCGGATGAGATGACATCAGAAAGCAGAGCTCTCGAGACAGCAAAAGATGC 120

QY 996 tgaatgtaagaagcgccgcttgcgtcagaacacacatgcatccagatgacatccaa 1055
|||||
Db 121 TGATGTACAGACGCGCTTCCTTCGTACGAACACACATGCATCCAGATGCATCCATCAA 180

QY 1056 gaacgaagatccccagatgataacttactccagtgaggcgctgagactta 1115
|||||

Db 181 GAAAGAGATGCCAGATGATGATGATTACTTACACAGTAAGGGCGGTGAGACTTA 240

QY 1116 tgaatgcttltgaagatcaaagagtccttggaaactatgacgtaccttctcagcaac 1175
|||||
Db 241 CGAAATCTCTGTGAAGATCAAAAGATCCCTGGAACTCATGCAGTCTCTCCAGCAC 300

QY 1176 aattgaagctacagagcaagcagcagcagcagcagcagcagcagcagcagcagcagc 1215
|||||
Db 301 GATTGAACCTTACAGGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 360

QY 1236 ccttcagccttctcagaatgagcttggagcccgagagagaactccaacaac 1295
|||||
Db 361 CTTTTCAGCGCTTCGTTACGAGATGAGCTTGTGAGACCGCGGAGAGAAACCCGAGACATC 420

QY 1296 tgaagcttctttagacattccaaagcccc 1325
|||||

Db 421 TGACGCTCTTTAGACATTCACGTCCGCC 450

RESULT 8
AM379296 508 bp mRNA EST 04-FEB-2000
LOCUS AM379296
DEFINITION MRO-HT0241-091299-004-b02 HT0241 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM379296
VERSION AM379296.1 GI:6883955
KEYWORDS EST.
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 508)
HCGP http://www.ludwig.org.br/ORESSES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
JOURNAL
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MRO&t=MRO-HT0241-
091299-004-b02&t3=1999-12-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 72
High quality sequence stop: 438.
Location/Qualifiers
1. 508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0241"
/dev_stage="adult"
/note="Organ: head,neck; Vector: puc18; Site.1: SmaI;
Site.2: SmaI; A mini-library was made by cloning products
derived from ORESSES PCR (U.S. Letters Patent application
No. 196/716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 154 a 116 c 131 g 107 t
ORIGIN

Query Match 30.2%; Score 405.6; DB 115; Length 508;
Best Local Similarity 93.3%; Pred. No. 6.7e-104;
Matches 446; Conservative 0; Mismatches 29; Indels 3; Gaps 2;

QY 758 caccacagttggcagcgaattcagacagctctgtacaatt--tcattgttaacagag 815
|||||
Db 3 CACCTCTGAGTGGACATGAATTCATGACAGGCTTGTACACATGACATGTGTAAACACAG 62

| BASE COUNT | 117 a | 135 c | 146 g | 171 t | ORIGIN |
|-----------------------|-----------------|--|------------|-------------|--------|
| Query Match | 29.2% | Score 393; | DB 118; | Length 569; | |
| Best Local Similarity | 97.2%; | Pred. No. 2,6e-100; | | | |
| Matches 415; | Conservative 0; | Mismatches 0; | Indels 12; | Gaps 1 | |
| Db | 559 | GTACACAGCATGTTGTTGTGGAGGAGATGACCGCGGTCACATTATATCTTTTACTTGG | 510 | | |
| Qy | 866 | aaacacagagatgggcgaagctctcttggcgccgctgtctttgaaagcccgagctcgtgtgtcc | 925 | | |
| Db | 509 | AAACACAGATGGCCANAGTCTGCGCCGCGCTGCTTTGAGCCCGCATCTGTGCTTGCC | 450 | | |
| Qy | 926 | caggaaagacacaggaagcgagctgaagatgacatcagaagaacgaagatttcgaaacgta | 985 | | |
| Db | 449 | CAGGAAGAGACAGGAAGCGGATGAAGATACATCAGAAACACCAAGTTTCGACACGTA | 390 | | |
| Qy | 986 | caaaagacggttgatgtgtaagaagcgccggttcgttcagaacacacatggtatccaaatga | 1045 | | |
| Db | 389 | CAAAAGAACGGTGATG-----GGTTTCGTCAGAAACACATGATATCCAGATGA | 342 | | |
| Qy | 1046 | catcatcacaagaagaagatcccagatgtgaactgttatacttaccaggtgaagggcc | 1105 | | |
| Db | 341 | CATTCATCAAGAAACGAAACATCCCAAGATGATGAACTGTTACTTTCACAGTAGAGGGCC | 282 | | |

[illegible]

| RESULT | 10 |
|--------------|-------------|
| LOCUS | AK017412 |
| AK017412 | |
| Mus musculus | 2045 bp |
| musculi | 6 days |
| regulator | head |
| embryo | 10 days |
| HTC | 08-FEB-2001 |

| | |
|-----------|--|
| ACCESSION | 110141.y, clone:54304339E07, full insert sequence. |
| VERSION | AK017412.1 |
| KEYWORDS | AK017412.1 GI:12856635 |
| SOURCE | CAP trapper. |
| | Mus musculus (strain:C57BL/6J) 6 days neonate head cDNA to mRNA, |
| | clone_11b:RKEN full-length enriched mouse cDNA library |
| | clone:54304339E07. |
| ORGANISM | Mus musculus |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| AUTHORS | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| TITLE | 1 (sites) |
| JOURNAL | Carninci, P. and Hayashizaki, Y. |
| | High-efficiency full-length cDNA cloning |
| | Methods Enzymol. 303, 19-44 (1999) |

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS

2 (sites)
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalisation and subtraction of cap-trapper selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome. Res. 10 (10), 1617-1630 (2000)
20499374

3 (sites)
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Kikuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T.,
Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T.,
Kashiwagi, K., Fujiwara, S., Inoue, K., Todawa, Y., Iizawa, M., Chazotte, P.,
Kobayashi, M., and Hayashizaki, Y. (2000) A full-length cDNA library
prepared by cap-trapper method for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

| TITLE | JOURNAL | MEDLINE REFERENCE | AUTHORS |
|---|--|--|----------|
| Matsura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y. | Riken Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer | Genome Res. 10 (11), 1757-1771 (2000) | 20530913 |
| 4 (sites) | The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium. | Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5 (bases 1 to 2045) | |
| Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Futuno, M., Hanagaki, T., Hara, A., Hayashi, N., Hiramoto, K., Hirokawa, T., Horii, F., Imoto, Y., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kuilhara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numasaki, R., Ono, M., Okazaki, Y., Oshida, T., Owa, C., Saio, H., Saio, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shiba, Y., Shimagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, H., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. | Direct Submission | Submitted (10-JUL-2000) | |
| Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, url: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216) | Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. | CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAAGACGATCCAGAGCTCCTCTTTTATTATTTTAA 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAAGATTCGTGCATTAATAATTAATCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI, 3' end: BamBI. Host: DH10B. | |
| Location/Qualifiers | | | |
| I. 2045 | /organism="Mus musculus" | | |
| | /strain="C57BL/6J" | | |
| | /db_xref="taxon:10090" | | |
| | /db_xref="MGI:1336991" | | |
| | /db_xref="MGD:MGI:1897119" | | |
| | /clone="5430439E07" | | |
| | /tissue_type="head" | | |
| | /clone_lib="RIKEN full-length enriched mouse cDNA library" | | |
| | /dev_stage="6 days neonate" | | |
| <1. 1545 | /note="putative" | | |
| | /codon_start=1 | | |
| | /protein_id="BAB30732.1" | | |
| | /db_xref="GI:12856636" | | |
| | /translation="DFEVTFQOOSCTKASATWPTSLKLKYCOIAFKCPIDIQSTPPPCPGATRAMPVYKKAEHVDTIVRCRNHELGDRNEGOASPAHLIVEGNLRAQVDDPYGRSVAVPPEPPOGVTEFTTLINFCNNSCVGMNRPLVTITLETROGVLVGRSFEGRICAPGRDRKADEHVRQOALNESTTKNGAASKAFKSPAIPLGTVN VKRRRHODEDMFYMHVGRNFELIMKVEKLSLEMLVLPVLVDYSKOQOOQLORPP SHLOPPEYGPVLSPMNKVGAVGSKLPVNOLVGGPPHSSAGCNLDPMGSGMNSGSHSMFANGENGSHSSOTMSGTPPTPPHADPSISFLTGACCGICTCFSTGSGLO SIYHLAKLTIEDLCALKVPPOYKNRTIKRGIDLQKSHDCGQILRSSMAATJISGGS GELORSVMFAVFRVHRHTTIIPRGAGAVTGPDEWADGFELDLPDKSRKPKEEF TELESH" | | |

| | | | | | | | | | |
|------------|--|--|--------------------|-----------------|--------------|--------|--|--|--|
| | BASE COUNT | 465 a | 629 c | 543 g | 408 t | | | | |
| | ORIGIN | | | | | | | | |
| | Query Match | 29.0%; | Score 390.2; | DB 192; | Length 2045; | | | | |
| | Best Local Similarity | 68.1%; | Pred. No. 2.3e-99; | | | | | | |
| | Matches 577; | Conservative | 0; | Mismatches 258; | Indels 12; | Gaps 2 | | | |
| OY | 412 | ttcgacgtgctcttcaccagcagtcgacgcgcgaagtgcggccactgtagcattccact | 471 | | | | | | |
| DB | 4 | TTGCGAGTCCACTTCACGACGTGCAGCACTGCCAAGTCGGCACCTGGACATCATC | 63 | | | | | | |
| OY | 472 | gaactgaagaacctactatgcaccaatttgaagaacatgcccccatacagatcaagtatg | 531 | | | | | | |
| DB | 64 | CTCTGAAGAAGATTGTACTGTCTAGATTGCTTAAGACATGGCCCATCCAGATCAAAGTG | 123 | | | | | | |
| OY | 532 | accaccacccccccaaggagctgttatccgcgcatacgccgtctacaaaaagctgagcac | 591 | | | | | | |
| DB | 124 | ACACACACACCCCCGGGCGACGGCCATCCGGGCGCATGCTGTACAGAAAGCAGAGCAT | 183 | | | | | | |
| OY | 592 | gtcacgagagtggtgaagcgtgtgccccaaca ttgactgtagccgtgaattcaacagagga | 651 | | | | | | |
| DB | 184 | GTGACCGCATTTGTTAAAGGCTGCCCCAACACACAGAGCTTGGAAAGGAGACTTCATGAAGA | 243 | | | | | | |
| OY | 652 | cagattgccctcctctagtcattgatctgagtagagggagacaccatgcccagtatgta | 711 | | | | | | |
| DB | 244 | CAGTGTGCCCCCGGTAGCCACCTCATCCGTGTAGAAGGCAACAACCTCCGCAATGACGTG | 303 | | | | | | |
| OY | 712 | gaagatccatatcacaggaaagagagtggtgtgtacttaacctaagacccaggttggc | 771 | | | | | | |
| DB | 304 | GATGACCCTGTACCGGAAGGCAAGATGTTGGTTGTCCCTATAAGAACCCCACACAGGGGGA | 363 | | | | | | |
| OY | 772 | actgaattcaacagactctgtfacaaattccaatgtgtgaacagagtgltgttgagagga | 831 | | | | | | |
| DB | 364 | ACAGATTATTACACCATCCTGTACCACTTCATGTGTAAACAGCAGCTGTGGGGGGCATG | 423 | | | | | | |
| OY | 832 | aacgcgcgtccaattltaactatgttactctgtgaacacagagatgggcaagtcctgggc | 891 | | | | | | |
| DB | 424 | AATCCGAGGCCCCATCTGTCTCATATCACCCCTGGAGACCCGGGATGGACAGGCTCTGGGC | 483 | | | | | | |
| OY | 892 | cgaagctgcttggaagcccgagatcgtgtgtcccaaggaaagagacagaggcgaatga | 951 | | | | | | |
| DB | 484 | CGCCGGTCTTTGAGGGGTGCATCTGTGCTCTGCTCCGCGGTGACCGCAAGCTGATGAA | 543 | | | | | | |
| OY | 952 | gataagatcagaagaagcaagtttcoga-----cagtacaaaagaacgltatgtlacg | 1005 | | | | | | |
| DB | 544 | GACCATTTACGGGGAGACCAACAGGCTCTGATGTGAAGTAGAACCAAAAATGTGACTGGCAC | 603 | | | | | | |
| OY | 1006 | aagcgcccgcttcgttcagacacacatglat----ccagaatgacatcalcataangaa | 1059 | | | | | | |
| DB | 604 | AAACGTGCATTCACAGAGAGCCCGCTGCCATCCGCTGGGTATCCAACTGTAAGGAAG | 663 | | | | | | |
| OY | 1060 | cgaagaatccccagatgataactgttatatacttaccagltgaggggcgtgtagactatgaa | 1119 | | | | | | |
| DB | 664 | AGACCCCAAGGGGAGAGACATGTTATCATGACAGTCCGAGGCGGGAGAACCTTTGAG | 723 | | | | | | |
| OY | 1120 | atcgctgttgaagaataaagaagtcctctggaactcatgacagctactcttcctacacacaact | 1179 | | | | | | |
| DB | 724 | ATCTTGATGAAGTAGTCAAGGAGAGCCTAGAACCTGATGATGAGACTTGTCGCCCTTTGGTT | 783 | | | | | | |
| OY | 1180 | gaaagatcaaggaacacagcaaacagcagcagcagcagcagcacttacttaagaanaatcctt | 1239 | | | | | | |
| DB | 784 | GACCTCTTGCAGACAGCAGCAGCAGCAGCAGCAGCTCTTACAGAGCCGAGTCACTGACGCT | 843 | | | | | | |
| OY | 1240 | tcaagcct 1246 | | | | | | | |
| DB | 844 | CCATCCT 850 | | | | | | | |
| <hr/> | | | | | | | | | |
| RESULT 11 | | | | | | | | | |
| AM379300 | 565 bp | mRNA | EST | 04-FEB-2000 | | | | | |
| LOCUS | | | | | | | | | |
| DEFINITION | MR0-HT0241-101299-003-e05 HT0241 Homo sapiens CDNA, mRNA sequence. | | | | | | | | |

| | Query Match | 27.1% | Score 364.4 | DB 115 | Length 507 |
|----|-----------------------|---|-------------------|---------------|------------|
| | Best Local Similarity | 92.8% | Pred. No. 3.2e-92 | | |
| | Matches 464 | Conservative | 0 | Mismatches 16 | Indels 20 |
| | | | | Gaps 7 | |
| QY | 572 | tctcaaaaaagctgcagcagctcaacgaggtgtgttaagcagtggtcccaacatcagagctga | 631 | | |
| Db | 20 | TCTCAAAAAGGTGTGACACGTCACGGGGGTGTGTACGCGGTGCCCAACCMAGACTCTA | 79 | | |
| QY | 632 | gcgcgtgaattcaacgagggagacagattgcacctctagtcaattgattcaagatgaaggaga | 691 | | |
| Db | 80 | GCGCTGAATTCAACGAGGACAGATTGCCCTCTCTAGTCAATTGATTCAAGTAGAGGGGA | 139 | | |
| QY | 692 | acagacatgccacagatgatgaagaatcccatcaacaagaagaacagagttgctggttaacct | 751 | | |
| Db | 140 | ACAGCATATCCCATGATGTAGACAGTCCATCMACAGAAACACAGATGTGCGTGACTT | 199 | | |
| QY | 752 | atgaagcaccaccagtttggcactgaattc-acgaacgctctgtac-aattcaatgtgtaa | 809 | | |
| Db | 200 | ATGAGCACCCCAAGCTTGGCACTTAAATTCCTTCTTCTTCTTCTTCTTCTTCTTCTT | | | |

| Query Match | Best Local Similarity | Matches | 378: Conservative |
|-------------|--------------------------------|---------------------------|-------------------------------------|
| 27.0% | Score 363; DB 139; Length 541; | 93.8%; Pred. No. 8,1e-92; | 0; Mismatches 25; Indels 0; Gaps 0; |

| FEATURES | source |
|--|--|
| ORGANISM | Bos taurus |
| LOCUS | BE752074 541 bp mRNA |
| DEFINITION | 204371 MARC 2B0V Bos taurus cDNA 5', mRNA sequence. |
| ACCESSION | BE752074 |
| VERSION | BE752074.1 GI:10166066 |
| KEYWORDS | EST. |
| SOURCE | cow. |
| ORGANISM | Bos taurus |
| LOCUS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos. |
| REFERENCE | 1 (bases 1 to 541) |
| AUTHORS | Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid,W.W. and Keeler,J.W. |
| TITLE | Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle |
| COMMENT | Unpublished (2000) |
| CONTACT | Contact: Smith TPJ |
| USDA, ARS, US Meat Animal Research Center | PO Box 166, Clay Center, NE 68933-0166, USA |
| Tel: | 402 762 4366 |
| Fax: | 402 762 4390 |
| Email: | smitht@mail.marc.usda.gov |
| Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options. | |
| PCR primers | |
| FORWARD: AGGAAACGCTATACCAT | |
| BACKWARD: GTTTCACAGTCAGACG | |
| Plate: 45 | row: M column: 16 |
| Seq primer: ATTAGGTGACATCTATAG | |
| Location/Qualifiers | |
| 1..541 | |
| /organism="Bos taurus" | |
| /db_xref="taxon:9913" | |
| /clone_id="MARC 2B0V" | |
| /tissue_type="pooled" | |
| /lab_host="DH10B" | |
| /note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI; library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium." | |
| BASE COUNT | 149 a 132 c 133 g 127 t |
| ORIGIN | |

[illegible]

